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OM protein - protein search, using sw model

Run on: November 16, 2005, 16:22:56 ; Search time 103.05 Seconds
(without alignments)
743.120 Million cell updates/sec

Title: US-09-575-580B-4
Perfect score: 1048
Scoring table: BLOSUM62
Gapext 0.5

Sequence: 1 MEEYDLDLPSATTACHLDP.....RPKKIQTRRPPYPTPLHS 198

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing First 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqP1980s:*
- 2: geneseqP1998s:*
- 3: geneseqP2000s:*
- 4: geneseqP2001s:*
- 5: geneseqP2002s:*
- 6: geneseqP2003as:*
- 7: geneseqP2003bs:*
- 8: geneseqP2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1048	AEE18911 Human MC1	100.0	198	5	AAE18911	Aee18911 Human MC1
2	1002.5	AEE18915 Human MC1	95.7	197	5	AAE18915	Aae18915 Human MC1
3	1002.5	Adr14119 Human NF-	95.7	197	8	ADR14119	Adr14119 Human NF-
4	1002.5	Adb64738 Human pro	95.7	252	7	ADB64738	Adb64738 Human pro
5	920.5	Aee18912 Mouse MC1	87.8	198	5	AAE18912	Aae18912 Mouse MC1
6	872.5	Aee18914 Human MC1	83.3	197	5	AAE18914	Aae18914 Human MC1
7	872.5	Adz25770 Human pro	83.3	197	7	ADZ25770	Adz25770 Human pro
8	842.5	Adr10481 Human pro	80.9	242	2	ADR10481	Adr10481 Human pro
9	835.5	Aaw73898 Human Dow	79.7	171	2	AAW73898	Aaw73898 Human Dow
10	620.5	Aab31788 Amino aci	59.2	234	4	AAB31788	Aab31788 Amino aci
11	620.5	Adb64062 Human Dow	59.2	243	7	ADB64062	Adb64062 Human Dow
12	620.5	Aam50760 Human Dow	59.2	255	5	AAM50760	Aam50760 Human Dow
13	620.5	Adz37339 Human Dow	59.2	255	7	ADZ37339	Adz37339 Human Dow
14	613.5	Aae18913 Mouse MC1	58.5	197	5	AAE18913	Aae18913 Mouse MC1
15	609.5	Abd07172 Human P53	58.2	197	6	ABD07172	Abd07172 Human P53
16	596.5	Aae18916 Human MC1	56.9	192	5	AAE18916	Aae18916 Human MC1
17	596.5	Ade37341 Human Dow	56.9	192	5	ADE37341	Ade37341 Human Dow
18	596	Aee18917 Human MC1	56.9	241	5	AAE18917	Aae18917 Human MC1
19	596	Abo07173 Human P53	56.9	241	6	ABO07173	Abo07173 Human P53
20	596	Ade37342 Human Dow	56.9	241	5	ADE37342	Ade37342 Human Dow
21	595	Aae18918 Human MC1	56.8	212	5	AAE18918	Aae18918 Human MC1
22	497	Aab88452 Lung canc	47.4	142	3	AAB88452	Aab88452 Lung canc
23	439	AAG01768 Human sec	41.9	111	4	AAG01768	AAG01768 Human sec
24	379.5	Abb71467 Drosophil	36.2	292	4	ABB71467	Abb71467 Drosophil
25	284	Aam15671 Peptide #	27.1	58	4	AAM15671	Aam15671 Peptide #

ALIGNMENTS

RESULT 1
ID AAE18911 standard; protein; 198 AA.
XX AC AAE18911;
XX DT 17-MAY-2002 (First entry)

XX DE Human MCIP associated protein #2.

XX KW Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;

XX heart failure; cardiomyopathy; heart disease; human.

XX Homo sapiens.

XX OS Homo sapiens.

XX PN WO200204491-A2.

XX PD 17-JAN-2002.

XX PF 06-JUL-2001; 2001WO-US021662.

XX PR 07-JUL-2000; 2000US-021661P.

XX PR 13-FEB-2001; 2001US-00782353.

XX PA (TEXA) UNIV TEXAS SYSTEM.

PA (WILLI /) WILLIAMS S. R.

PA (ROTH /) ROTHERMEL B.

XX PI Williams SR, Rothermel B;

XX XX WPI ; 2002-179698/23.

DR N-PSDB; AAB30152.

XX Disclosure; Page 148-149 ; 174pp; English.

XX Screening for modulators of muscle calcineurin interacting protein (MCIPs)

PT binding, expression or phosphorylation, useful for treating cardiac

CC and nucleic acid molecules encoding such proteins. MCIPs form a physical

CC complex with the catalytic subunit of calcineurin and increased levels of

CC MCIPs correspond to a reduced ability of calcineurin to stimulate

CC transcription of certain target genes. The invention also relates to

CC methods for identifying modulators of MCIP binding, expression or

CC phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin

CC may be used for treating cardiac hypertrophy and heart failure.

CC Antibodies to MCIP can be used in characterising the MCIP content of healthy and diseased tissues and subsequently for determining the presence or absence of cardiomyopathy or as predictor of heart disease.

CC The present sequence is human MCIP associated protein

XX Sequence 198 AA;

Query Match 100.0%; Score 1048; DB 5; Length 198;
Best Local Similarity 100.0%; Pred. No. 7.3e-108;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEYVDLQDLPSSATIACHLDPRVFDGLCRAKFSSLFRYDKDTTFOYFKSFKVRINFSN 60
Db 1 MEYVDLQDLPSSATIACHLDPRVFDGLCRAKFSSLFRYDKDTTFOYFKSFKVRINFSN 60
Qy 61 PLSAADARLRLHKTFLGKEMKLYFAQTTHIGSSHLLAPPNPDKQFLISPPVGWIKQV 120
Db 61 PLSAADARLRLHKTFLGKEMKLYFAQTTHIGSSHLLAPPNPDKQFLISPPVGWIKQV 120
Qy 121 EDATPVINYDLIYAISKGKGEKYLEHAATDPPPSVYVHVCESDOENEEREEEMERNKRP 180
Db 121 EDATPVINYDLIYAISKGKGEKYLEHAATDPPPSVYVHVCESDOENEEREEEMERNKRP 180
Qy 181 KPKIQTTRPEYTPHLS 198
Db 181 KPKIQTTRPEYTPHLS 198

RESULT 2
APB18915 standard; protein; 197 AA.

ID APB18915
ID ADR14119 standard; protein; 197 AA.

XX DT 17-MAY-2002 (first entry)

DB Human MCIP associated protein #2.

XX KW Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;

KW heart failure; cardiomyopathy; heart disease; human.

XX OS Homo sapiens.

XX PN WO200204491-A2.

XX PD 17-JAN-2002.

XX PF 06-JUL-2001; 2001WO-US021662.

XX PR 07-JUL-2000; 2000US-0216601P.

PR 13-FEB-2001; 2001US-00782933.

XX (TEKA) UNIV TEXAS SYSTEM.

PA (WILL /) WILLIAMS S R.

PA (ROTH /) ROTHERMEL B.

XX PT Williams SR, Rothermel B;

XX WPI; 2002-179698/23.

DR N-PSDB; AAD30156.

XX Screening for modulators of muscle calcineurin interacting protein (MCIP)

PR binding, expression or phosphorylation, useful for treating cardiac

PR hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a

test compound.

XX Example 1; Page 161-162; 174pp; English.

CC The invention relates to muscle calcineurin interacting proteins (MCIPs) and nucleic acid molecules encoding such proteins. MCIPs form a physical complex with the catalytic subunit of calcineurin and increased levels of MCIPs correspond to a reduced ability of calcineurin to stimulate transcription of certain target genes. The invention also relates to

CC methods for identifying modulators of MCIP binding, expression or phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin CC may be used for treating cardiac hypertrophy and heart failure.

CC Antibodies to MCIP can be used in characterising the MCIP content of healthy and diseased tissues and subsequently for determining the presence or absence of cardiomyopathy or as predictor of heart disease.

CC The present sequence is human MCIP associated protein. Note: This sequence has been described as murine MCIP splice variant in the CC specification, however the sequence seems to be a MCIP associated protein

CC XX specification, however the sequence seems to be a MCIP associated protein

CC SQ Sequence 197 AA;

CC SQ Query Match 95.7%; Score 1002.5; DB 5; Length 197;

CC SQ Best Local Similarity 96.5%; Pred. No. 8.4e-103; Mismatches 3; Indels 1; Gaps 1;

CC SQ Matches 191; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

CC Qy 1 MEEVDLQDLPSSATIACHLDPRVFDGLCRAKFSSLFRYDKDTTFOYFKSFKVRINFSN 60

CC Db 1 MEEVDLQDLPSSATIACHLDPRVFDGLCRAKFSSLFRYDKDTTFOYFKSFKVRINFSN 60

CC Qy 61 PLSAADARLRLHKTFLGKEMKLYFAQTTHIGSSHLLAPPNPDKQFLISPPVGWIKQV 120

CC Db 61 PLSAADARLRLHKTFLGKEMKLYFAQTTHIGSSHLLAPPNPDKQFLISPPVGWIKQV 120

CC Qy 121 EDATPVINYDLIYAISKGKGEKYLEHAATDPPPSVYVHVCESDOENEEREEEMERNKRP 180

CC Db 121 EDATPVINYDLIYAISKGKGEKYLEHAATDPPPSVYVHVCESDOENEEREEEMERNKRP 180

CC Qy 181 KPKIQTTRPEYTPHLS 198

CC Db 181 KPKIQTTRPEYTPHLS 198

CC Qy 180 KPKIQTTRPEYTPHLS 197

CC Db 180 KPKIQTTRPEYTPHLS 197

CC RESULT 3
ADR14119
XX ID ADR14119 standard; protein; 197 AA.
AC ADR14119;

CC XX DT 21-OCT-2004 (first entry)

CC XX DE Human NF-kappaB pathway-associated protein SeqID120.

CC XX NP-NF-kappaB pathway; antiinflammatory; cytostatic; hepatotoxic; virucide;

CC KW antiarthritic; antirheumatic; Gastrointestinal-Gen; antiastmatic;

CC KW antarteriosclerotic; immunoprotective; vasotropics;

CC KW immunosuppressive; pulmonary; gene therapy; immune disorder;

CC KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;

CC KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;

CC KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;

CC KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;

CC KW viral infection; HIV-1; HTLV-1; hepatitis C; BBV; influenza;

CC KW viral replication; host cell survival; evasion of immune response;

CC KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;

CC KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;

CC KW autoimmune disorder; hyper immune activity;

CC KW aberrant acute phase response; hypercongenital condition; birth defect;

CC KW necrotic lesion; wound; organ transplant rejection; cancer;

CC KW aberrant signal transduction; proliferating disorder; cancer;

CC XX Homo sapiens.

CC XX PN WO2004065577-A2.

CC XX DT 05-AUG-2004.

CC XX DE Human NF-kappaB pathway-associated protein SeqID120.

CC XX OS Homo sapiens.

CC XX PN WO2004065577-A2.

CC XX DT 13-JAN-2004; 2004WO-US000798.

CC XX PR 14-JAN-2003; 2003US-0440068P.

CC XX PR 12-MAY-2003; 2003US-0469757P.

CC XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX	Nadler SG, Neubauer MG, Feder JN, Carman J;	KW Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration; cell regeneration; membrane protein; signal transduction related protein; cancer; tumour.
XX	WPI: 2004-562168/54.	KW
DR	N-PSDB; ADR14118.	KW transcription-related protein; osteoporosis; neurological disease;
XX		XX
PT	New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway.	OS Homo sapiens
PT		XX
PT		PN EP1308459-A2.
XX	Claim 6; SEQ ID NO 120; 237bp; English.	XX
XX	This invention relates to the novel association of protein sequences (and the genes which encode them) to the NF-kappaB pathway. The invention may be useful for the production of compounds with an antiinflammatory, antirheumatic, cyrostatic, hepatotropic, virucide, antiarrhythmic, antiarthritic, gastrointestinal, cerebroprotective, vasotrophic, immunosuppressive or immunomodulator, antiasthmatic, antiarteriosclerotic, vulnerary activity or for gene therapy. The proteins and nucleotides are useful for diagnosing, preventing, treating, or ameliorating conditions or diseases associated with the NF-kappaB pathway. The condition is an immune disorder, an inflammatory disorder, an aberrant NF-kappaB pathway, an aberrant NF-kappaB regulation, cancer, aberrant apoptosis, hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM syndromes, hypohidrotic ectodermal dysplasia, X-linked arachidotic ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1, hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell survival, evasion of immune responses, rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper immune activity, disorders related to aberrant acute phase responses, hypercongenital conditions, birth defects, necrotic lesions, wounds, organ transplant rejection, conditions related to organ transplant rejection, disorders related to aberrant signal transduction, proliferating disorders, cancers and HIV propagation in cells infected with other viruses. The present sequence is that of a human protein which is subject to the novel association with the NF-kappaB pathway of the invention. Note: This sequence does not appear in the specification but was obtained by the indexer from Genbank.	XX
XX	Sequence 197 AA;	XX
Query	Match 95.7%; Score 1002.5; DB 8; Length 197; Best Local Similarity 96.5%; Pred. No. 8.e-103; Mismatches 3; Indels 1;	XX
Db	1 MEEVDLQDPLSATIACHLDPRVFVDGLCRAKPESLPRTYDQTKTQFSKRVRINFSN 60 1 MEEVDLQDPLSATIACHLDPRVFVDGLCRAKPESLPRTYDQTKTQFSKRVRINFSN 60	XX
Query	61 PLSAADARLRLHKTBFGLGKMLYFAQTHIGSSHLAPPNDPKFLISPPASPPVGWIKQV 120 61 PLSAADARLQLHKTBFGLGKMLYFAQTHIGSSHLAPPNDPKFLISPPASPPVGWIKQV 120	XX
Db	121 EDATPVINYDLLYAIISKIGLGKGEYKLHATDTPPSVWVHCSDQENBEBEMERKRP 180 121 EDATPVINYDLLYAIISKIGLGKGEYKLHATDTPPSVWVHCSDQEBEBEMERKRP 179	XX
Query	181 KPKIIQTRRPEYPTIHL 198 180 KPKIIQTRRPEYPTIHL 197	XX
Db	RESULT 4 ADB64738 ID ADB64738 standard; protein; 252 AA. XX AC ADB64738; DT 04-DEC-2003 (first entry) DE Human protein encoded by clone NT2NEE2014040. XX	XX
Query	Match 95.7%; Score 1002.5; DB 7; Length 252; Best Local Similarity 96.5%; Pred. No. 1.2e-102; Mismatches 3; Indels 1; Gaps 1;	XX
Db	1 MEEVDLQDPLSATIACHLDPRVFVDGLCRAKPESLPRTYDQTKTQFSKRVRINFSN 60 56 MEEVDLQDPLSATIACHLDPRVFVDGLCRAKPESLPRTYDQTKTQFSKRVRINFSN 115	XX
Query	61 PLSAADARLRIKTEFLGKEMLYFAQTLHIGSSHLAPPNDPKFLISPPASPPVGWIKQV 120	XX
Db	116 PLSAADARLQLHKTBFGLGKMLYFAQTLHIGSSHLAPPNDPKFLISPPASPPVGWIKQV 175	XX
Query	121 EDATPVINYDLLYAIISKIGLGKGEYKLHATDTPPSVWVHCSDQENBEBEMERKRP 180	XX

QY	11 SATTACHLDPRVYDGLCRAKFESSLFRTRYDKDTFOYFKSFKRVRINTSNPLSAADARL 70	CC compounds to identify at least one ligand which specifically binds a protein, for purifying a ligand from a sample for making a antibody. The foam cell-expressed nucleic acids are useful for diagnosing a cardiovascular disorder. The foam cell-expressed nucleic acids are useful as elements on a microarray which can be used for detecting related polymers in a sample, diagnosing cardiovascular disease, atherosclerosis. The present sequence represents a protein differentially expressed in LPS treated foam cells.
Db	11 SSUJACVNSDIFSESETRAKFESSLFRTRYDKDTFOYFKSFKRVRINTSNPLSAADARL 70	CC
QY	71 LHKTBEFLGKEMKL YFAQTTHIGSSHLAPNPDKQFLISPPASPVGMQVEDATPVINYD 130	CC
Db	71 LHKTBEFLGKEMKL YFAQTTHIGSSHLAPNPDKQFLISPPASPVGMQVEDATPVINYD 130	CC
QY	131 LLYAISKLGPGKEXYELHAATDTPSPVVHVVCESDQE-KEEEBEMMERMRPKLIIQTRP 190	XX
Db	131 LLYAISKLGPGKEXYELHAATDTPSPVVHVVCESDQE-KEEEBEMMERMRPKLIIQTRP 189	XX
QY	191 EYTPHLS 198	Sequence 197 AA;
Db	190 EYTPHLS 197	Query Match 83.3%; Score 872.5; DB 7; Length 197; Best Local Similarity 89.4%; Prdt. No. 2.5e-88; Matches 168; Conservative 7; Mismatches 12; Indels 1; Gaps 1;
RESULT 7		
ID	ADB25770 standard; protein; 197 AA.	QY 11 SATTAICHLDPRTVYDGLCRAKFESSLFRTRYDKDTFOYFKSFKRVRINTSNPLSAADARL 70
XX	AC ADB25770	Db 11 SSUJACVNSDIFSESETRAKFESSLFRTRYDKDTFOYFKSFKRVRINTSNPLSAADARL 70
DT	29-JAN-2004 (first entry)	QY 71 LHKTBEFLGKEMKL YFAQTTHIGSSHLAPNPDKQFLISPPASPVGMQVEDATPVINYD 130
XX	DE Human protein differentially expressed in foam cells #47.	Db 71 LHKTBEFLGKEMKL YFAQTTHIGSSHLAPNPDKQFLISPPASPVGMQVEDATPVINYD 130
DE	KW Human; differential expression; foam cell; LPS; lipopoly saccharide;	QY 131 LLYAISKLGPGKEXYELHAATDTPSPVVHVVCESDQE-KEEEBEMMERMRPKLIIQTRP 189
XX	KW cardiovascular disease; atherosclerosis.	Db 131 LLYAISKLGPGKEXYELHAATDTPSPVVHVVCESDQE-KEEEBEMMERMRPKLIIQTRP 189
OS	Homo sapiens.	QY 191 EYTPHLS 198
XX	PN US2003194721-A1.	Db 190 EYTPHLS 197
PD	16-OCT-2003.	RESULT 8
XX	PP 18-SEP-2002; 2002US-00247671.	ADR10481 ID ADR10481 standard; protein; 242 AA.
XX	PR 19-SEP-2001; 2001US-0323784P.	XX ADR10481;
XX	PA (INCYT) INCYT GENOMICS INC.	XX DT 04-NOV-2004 (first entry)
XX	PT Mikita T, Shiffman D, Porter JG, Kaser MR;	XX Human protein useful for treating neurological disease Seq 3987.
XX	DR 2003-875398/81.	XX KW human; oligo-capping method; diagnostic marker; gene therapy;
DR N-PSDB; ADE25696.	XX DR Parkinson's disease; neurologic disease; Alzheimer's disease;	
PT Combination containing several polynucleotide that are differentially expressed in foam cells and complements of the polynucleotides, useful for diagnosing cardiovascular disease or atherosclerosis	XX KW sense or motor function; emotional reaction; fear response; panic; osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic; transmigriniser.	
XX Disclosure: SEQ ID NO 174; 37pp; English.	XX KW Homo sapiens.	
PS	XX	XX OS Homo sapiens.
XX	XX	XX PN EP1447413-A2.
CC	The invention relates to a combination comprising several polynucleotides having any one of 127 sequences (S1) such as the sequence of human calmodulin gene, human mRNA for KIAA0930 protein, leukotriene A4 hydrolase, human CGI-142 protein mRNA, human K+ channel beat 2 subunit mRNA, etc. and their complements. The cDNAs are differentially expressed in LPS (lipopolysaccharide) treated foam cells. Also included are obtaining an extended or full length gene from a library of nucleic acid sequences, an expression vector containing the nucleic acids, a host cell containing the vector, purified polypeptide appearing as ADE25750 and ADE25751, producing a protein by culturing the host cell, and a composition comprising a purified antibody that specifically binds to the proteins. The foam cell-expressed nucleic acids are useful for a high throughput detection of differential expression of one or more polynucleotides in a sample. The sample is from a subject with atherosclerosis and comprises in a standard defines early, mid or late stages of the disorder. The foam cell-expressed nucleic acids are useful for high throughout screening of a library of molecules or compounds to identify ligand which binds a polynucleotide. The library is chosen from DNA molecules, peptides, proteins and RNA molecules. The protein is useful for a high throughput screening of library of molecules or	XX PD 18-AUG-2004.
CC	CC	XX PF 12-FEB-2004; 2004EP-00003145.
CC	CC	XX PR 14-FEB-2003; 2003JP-00102207.
CC	CC	XX PR 09-MAY-2003; 2003JP-00131452.
CC	CC	XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.
CC	CC	XX PI Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Obuki T;
CC	CC	XX PI Wakamatsu A, Ishii S, Nagai K, Irie R;
CC	CC	XX DR WO 2004-563265/57.
CC	CC	XX DR N-PSDB; ADR10442.
CC	CC	XX PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's disease, Parkinson's disease, dementia and various cancers.
CC	CC	XX PS Claim 1; SEQ ID NO 3987; 268pp; English.
CC	CC	XX XX

XX XX Homo sapiens.
 PD XX BP1308459-A2.
 PF XX 06-JUL-2000; 20000WO-US018509.
 PR XX 07-JUL-1999; 99US-0142678P.
 PA (INCYT-) INCYTE GENOMICS INC.
 XX PA (HELI-) HELIX RES INST.
 PI PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 PT New human detoxification protein and polynucleotide, useful for
 PR diagnosis, prevention and treatment of autoimmune/inflammatory disorders
 PR and cell proliferative disorders including cancer.
 XX PS Claim 1; Page 77; 79pp; English.
 XX The present sequence represents a human detoxification polypeptide
 CC (DETX). DETX and its (anti)agonists are useful for preventing or treating
 CC disorders associated with decreased or increased expression or activity
 CC of DETX. DETX polypeptides are useful for screening compounds that
 CC specifically binds to DETX and for identifying (ant)agonists. Diseases
 CC prevented, treated and diagnosed include cancers (e.g. leukaemia,
 CC melanoma, adenocarcinoma, cancers of the brain, bone marrow, breast,
 CC kidney, liver, pancreas, prostate and uterus), autoimmune/inflammatory
 CC disorders (e.g. rheumatoid arthritis, asthma, atherosclerosis, autoimmune
 CC thyroiditis, psoriasis and ulcerative colitis), bacterial, fungal,
 CC parasitic infections and cell proliferative disorders (e.g. acrinic
 CC keratosis, arteriosclerosis, cirrhosis, and hepatitis). Anti-DETX
 CC antibodies may be used as antagonists, as a targeting or delivery
 CC mechanism for bringing pharmaceutical agents into contact with cells or
 CC tissues expressing DETX and for diagnosis of DETX-related disorders
 XX Sequence 234 AA;
 Query Match 59.2%; Score 620.5; DB 4; Length 234;
 Best Local Similarity 62.4%; Pred. No. 3 6e-60;
 Matches 121; Conservative 22; Mismatches 42; Indels 9; Gaps 2;
 Qy 5 DQDLPSTIACHLDPRVFDGLCRAKESLFRPTYDKDTTFQYFKSPKRVRINFNSPLSA 64
 Db 42 DFNDLPSLFACNHQSTYEGEESKEKEPGFLRPTYDDCTFQYFKSPKRVRINFNSPLSA 101
 Qy 65 ADARLRHKTEFLGKEMKLYPAQTHICSS---HIAAPNPDKQFLISPPSPVGKQV 120
 Db 102 ARARIELFETOPRGKKLMLYPAQVQTPTDGDKLHLAPQPAKQFLISPPSPVGWQPI 161
 Qy 121 EDATPVINYDLYIAISKGPGEKYELHATDPTPSVYHVCSDDQENEEEEREMMRKP 180
 Db 162 NDATPVINYDLYIAVAKIGPGEKYELHATDPTPSVYHVCSDDIEBEDPK---TSP 216
 Qy 181 KPKLICQTRPEXP 194
 Db 217 KPKLICQTRPEXP 230
 RESULT 1.1 ADB64052;
 ID ADB64052 standard; protein; 243 AA.
 XX AC
 XX DT 04-DEC-2003 (first entry)
 XX DE Human protein encoded by clone BRAWH20014590.
 XX KW Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
 KW cell regeneration; membrane protein; signal transduction-related protein;
 KW transcription-related protein; osteoporosis; neurological disease;
 KW cancer; tumour.

XX OS Homo sapiens.
 XX PN BP1308459-A2.
 XX PD 07-MAY-2003.
 XX PP 28-MAR-2002; 2002EP-00007401.
 XX PR 05-NOV-2001; 2001JP-00379298.
 XX PR 25-JAN-2002; 2002US-00350978.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshihikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX DR WBI; 2003-450961/43.
 DR N-PSDB; ADB62092.
 XX New polynucleotides and polypeptides, useful for developing a diagnostic
 PT marker or medicines for regulation of their expression and activity, or
 PT as targets of gene therapy.
 XX PS Claim 1; Page: 222pp; English.
 XX The invention discloses a polynucleotide comprising a sequence selected
 CC from 1970 fully defined nucleotide sequences which encode novel selected
 CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
 CC or its partial peptide, an antibody binding to the polypeptide or peptide
 CC of the polynucleotide, immunologically assaying the polypeptide or
 CC peptide of the polynucleotide by contacting the polypeptide or peptide
 CC with the antibody of the encoded protein, and observing the binding
 CC between the two, a transformant carrying the polynucleotide in an
 CC expressible manner and an antisense polynucleotide. The polynucleotide
 CC is useful as a primer for synthesising the polynucleotide, or as a probe
 CC for detecting the polynucleotide. The polynucleotides and encoded
 CC proteins are useful as pharmaceutical agents and many disease-related
 CC agents may be included in them, for developing a diagnostic marker or
 CC medicines for regulation of their expression and activity, or as targets
 CC of gene therapy. The genes are involved in tissue and/or cell
 CC regeneration. Membrane proteins, signal transduction-related proteins,
 CC transcription-related proteins, disease-related proteins and genes
 CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
 CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
 CC the activity or expression of the encoded protein to treat diseases. The
 CC sequence presented is a protein of the invention. Note: Some of the
 CC sequence data for this patent is not represented in the printed
 CC specification, but is based on sequence information supplied by the
 CC European Patent Office.
 XX SQ Sequence 243 AA;
 Query Match 59.2%; Score 620.5; DB 7; Length 243;
 Best Local Similarity 62.4%; Pred. No. 3.8e-60;
 Matches 121; Conservative 22; Mismatches 42; Indels 9; Gaps 2;
 Qy 5 DLQDLPSTIACHLDPRVFDGLCRAKESLFRPTYDKDTTFQYFKSPKRVRINFNSPLSA 64
 Db 51 DFNDLPSLFACNHQSTYEGEESKEKEPGFLRPTYDDCTFQYFKSPKRVRINFNSPLSA 110
 Qy 65 ADARLRHKTEFLGKEMKLYPAQTHICSS---HIAAPNPDKQFLISPPSPVGKQV 120
 Db 111 ARARIELFETOPRGKKLMLYPAQVQTPTDGDKLHLAPQPAKQFLISPPSPVGWQPI 170
 Qy 121 EDATPVINYDLYIAISKGPGEKYELHATDPTPSVYHVCSDDQENEEEEREMMRKP 180
 Db 171 NDATPVINYDLYIAVAKIGPGEKYELHAGTESTPSVYHVCSDDIEBEDPK---TSP 225
 Qy 181 KPKLICQTRPEXP 194

Db	226 KPKIQTTRPGLPP	239	Qy	65 ADARLRHKTEFLGKEMKLWFAQTLHIGSS - - - HIAAPPNPDQFLISPPASPPVGHQV 120
ID	AMM50760		Db	123 ARARIELHETQFRGKLUKLYFQVQTPTDGDKFLAPOPAAKQFLISPPSSPPVGHQPI 182
XX	AMM50760 standard; protein;	255 AA.	Qy	121 EDATPVINYDLIYASKLGPGEKYLHAAATDFTPSVYVHCESDQEENEEEREMERMRP 180
AC	AMM50760;		Db	183 NDATPVINYDLIYAVAKLGPGKYLHAGTSTPSVYVHVCDSDEEEEDPK---TSP 237
XX	18-APR-2002 (first entry)		Qy	181 KPKIQTTRPEYTP 194
DE	Human Down syndrome critical region 1-like 1 protein.		Db	238 KPKIQTTRPGLPP 251
XX	Down syndrome critical region 1-like 1; DSCR1L1 alpha; human;			
KW	Down syndrome; Alzheimer's disease; dementia; transgenic;			
KW	neuroprotective; nootropic; peptide therapy; gene therapy; Alzheimer's disease;			
XX	anticonvulsant; diagnosis; therapy.			
OS	Homo sapiens.			
XX				
FH	Key Location/Qualifiers			
FT	Misc-difference 1.			
FT	/note= "encoded by TNG"			
FT	Domain 129 . 199			
FT	/note= "nucleic acid binding domain"			
FT	Region 169 . 176			
FT	/note= "ISPXSSP box"			
XX	PN WO200204513-A2.			
XX	PD 17-JAN-2002.			
XX	PP 11-JUL-2001; 2001WO-US021982.			
XX	PR 11-JUL-2000; 2000US-00614474.			
XX	PA (INCYT-) INCYTE GENOMICS INC.			
XX	PI Loring JF, Tingley DW, Edwards CM, Streeter DG;			
XX	XX WPI; 2002-164633/21.			
DR	DR N-PSDB; ABA91457			
XX				
PT	Novel Down syndrome critical region 1-like 1 protein and nucleic acid encoding the protein useful for diagnosis and treatment of Alzheimer's disease, Down syndrome and other forms of dementia.			
PT	Claim 1: Page 47-49; 54pp; English.			
PS	The present sequence is that of novel Down syndrome critical region 1-like 1 protein (DSCR1L1 alpha). Northern analysis indicated expression of DSCR1L1 alpha in various libraries, with the highest abundance in tissues from the nervous system, including tissues associated with schizophrenia, Huntington's disease, epilepsy and amyotrophic lateral sclerosis. An absence of DSCR1L1 expression was observed in 7 of 8 libraries from subjects with Alzheimer's disease. A claimed method for detecting differential expression of a nucleic acid encoding DSCR1L1 alpha can be used to diagnose Down syndrome, Alzheimer's disease and other forms of dementia. The purified DSCR1L1 alpha protein, or a portion of it, can be used to identify ligands which specifically bind the protein, such as a DNA or RNA molecule, peptide nucleic acid, peptide, protein, mimetic, agonist, antagonist, antibody, immunoglobulin, inhibitor or drug, for use as a therapeutic. The protein can also be used to raise antibodies useful in diagnosis and therapy.			
XX	Sequence 255 AA;			
SQ	Query Match 5 DQDLPSPATIACHLDPRVFDGLCRAKPELSRPTYDKDTTOYFSKFRVRINFSNPLSA 64			
	Best Local Similarity 62.4%; Pred. No. 4.1e-60;			
	Matches 121; Conservative 22; Mismatches 42; Indels 9; Gaps 2;			
Qy	63 DNDLPLNSLFACNVHQSVFEGEBESKEFKERFEGFLRTYDDCCVTFQFLFSFRVINFNSPKSA 122			
Db	Query Match 59.2%; Score 620.5; DB 5; Length 255;			
	Best Local Similarity 62.4%; Pred. No. 4.1e-60;			
	Matches 121; Conservative 22; Mismatches 42; Indels 9; Gaps 2;			
Qy	Sequence 255 AA;			
Db	Query Match 59.2%; Score 620.5; DB 7; Length 255;			

CC contacting a cell defective in p53 function with a candidate modulator
 CC that specifically binds to a HM polypeptide comprising an HM amino acid
 CC sequence, where p53 function is restored), modulating (M3) a p53 pathway
 CC in a mammalian cell (comprising contacting the cell with an agent that
 CC specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)
 CC a disease in a patient (comprising: (a) obtaining a biological sample
 CC from the patient; (b) contacting the sample with a probe for HM
 CC expression; (c) comparing the results with a control; and (d) determining
 CC whether the comparison indicates a likelihood disease). (M1) is useful
 CC for identifying modulators of the p53 pathway. A probe for HM expression
 CC is useful for diagnosing breast, colon, kidney, lung and ovarian cancer,
 CC in a patient, where the cancer has greater than 25 % expression level.
 CC Modulators identified by (M1) are useful in a variety of diagnostic and
 CC therapeutic applications, where disease or disorder prognosis is related
 CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell
 CC proliferation disorders (e.g. cancer). Another two new methods (M2 and
 CC M3) are useful for modulating the p53 pathway of a cell, thus restoring
 CC the p53 function of the cell, so that the cell undergoes normal
 CC proliferation or progression through the cell cycle. (M2) and (M3) are
 CC also useful for treating defects in the p53 pathway such as angiogenic,
 CC apoptotic or cell proliferation disorders. The present sequence
 CC represents a human p53 pathway modifying protein
 XX

Sequence 197 AA;

Query	Match	Score	DB	Length
Best Local Similarity	58.2%	609.5;	DB 6;	Length 197;
Matches 119; Conservative	63.3%	Pred. No. 4.7e-59;		
	21;	Mismatches 39;	Indels 9;	Gaps 2;
Db	1.1 SATIACHILDPRVEVDGLCRAKFESLFRPTYDKOTTFQYFKSFKRVRINFSNPLSAADARLR 70			
Db	1.1 STLVACVVDVEFTNOEVKEKEPGLFRYYDCVTFOLFKSFRRVRINFSNPKSAADARIE 70			
Qy	71 LHKTIFLGKEMKLKPATQLHIGSS---HLAPPNPDKOFLISPPASSPVGKQVEDATPV 126			
Db	71 LHETQFRSKKLKPQATQTPEDGDKLHLAPPQAFLLSPSSPPVGHQPINDATPV 130			
Qy	127 INYDLLYAISKLGPGKELYELHATDPTPSVYVHVCESDQEENREEEEEMRKRPKDKIQ 186			
Db	131 LNDDLLAVAKLGPGEKELHAGTESTSFSVVVHVCDSDIEBBDPK---TSPKDKIQ 185			
Qy	187 TRRPEYTP 194			
Db	186 TRRPGLPP 193			

Search completed: November 16, 2005, 16:47:31
 Job time : 106.05 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	847.5	80.9	171	4 US-09-949-016-6493	Sequence 6493, Ap
2	847.5	80.9	173	4 US-09-949-016-11053	Sequence 11053, A
3	835.5	79.7	171	2 US-08-665-040-2	Sequence 2, Appli
4	620.5	59.2	255	4 US-09-614-474-2	Sequence 2, Appli
5	609.5	58.2	206	4 US-09-949-016-11450	Sequence 11450, A
6	596.5	56.9	192	4 US-09-614-474-10	Sequence 10, Appli
7	596.5	56.9	192	4 US-09-949-016-6659	Sequence 6659, Ap
8	596	56.9	241	4 US-09-614-474-11	Sequence 11, Appli
9	596	56.9	248	4 US-09-949-016-7081	Sequence 7081, Ap
10	439	41.9	111	4 US-09-513-999C-5849	Sequence 5849, Ap
11	372.5	35.5	289	4 US-09-270-767-4503	Sequence 44503, A
12	90.5	8.6	4019	4 US-09-854-133-425	Sequence 425, Appli
13	88	8.4	284	5 PCT-US94-09752-4	Sequence 4, Appli
14	8.3	8.22	4	US-09-824-734-3	Sequence 3, Appli
15	84.5	8.1	719	4 US-09-641-741-28	Sequence 28, Appli
16	83	7.9	367	4 US-09-248-796A-15492	Sequence 15492, A
17	82	7.8	1128	4 US-09-641-741-30	Sequence 8, Appli
18	82	7.8	1128	4 US-09-060-882-8	Sequence 2, Appli
19	81	7.7	1128	1 US-08-111-939-2	Sequence 2, Appli
20	80	7.6	314	2 US-09-328-52-524	Sequence 524, Ap
21	80	7.6	492	4 US-09-792-024-91	Sequence 91, Appli
22	79	7.5	708	4 US-09-949-016-5754	Sequence 7574, Ap
23	79	7.5	1132	1 US-08-446-038B-18	Sequence 18, Appli
24	79	7.5	1132	1 US-08-446-010B-18	Sequence 18, Appli
25	79	7.5	1132	2 US-08-805-445-18	Sequence 18, Appli
26	79	7.5	1132	2 US-09-066-208B-18	Sequence 18, Appli
27	79	7.5	1132	2 US-09-066-208B-18	Sequence 18, Appli

FILE REFERENCE: CLO01307
 CURRENT APPLICATION NUMBER: US/09/949, 016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241, 755
 PRIOR FILING DATE: 2000-10-00
 PRIOR APPLICATION NUMBER: 60/237, 768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231, 498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 11053
 LENGTH: 173
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-11053

Query Match 79.7%; Score 835.5; DB 2; Length 171;
 Best Local Similarity 94.7%; Pred. No. 1.9e-88;
 Matches 160; Conservative 5; Mismatches 3; Indels 1; Gaps 1;
 US-08-665-040-2

Qy 30 AKPESLFRTYDKDTFQYFSKFRVINFNSNPLSAADARLRLHKTEFLGKEMKLKPQTL 89
 Db 4 AKPESLFRTYDRDITFQYFSKFRVINFNSNPLSAADARLRLHKTEFLGKEMKLKPQTL 63

Qy 90 HIGSSHLLAPPNPDKQFLISPPASPPWQKVQEDATPVINYDLIYASKLGPGEKYELHAA 149
 Db 64 HIGSSHLLAPPNPDKQFLISPPASPPWQKVQEDATPVINYDLIYASKLGPGEKYELHAA 123

Qy 150 TDPTPSVYVHVCESDQEENEEBEMRMRKPKLQTTRREYTPHLS 198
 Db 124 TDPTPSVYVHVCESDQE-KEEEEMERMRKPKLQTTRREYTPHLS 171

RESULT 4
 US-09-614-474-2
 Sequence 2, Application US/09614474
 ; Patent No. 6524819
 ; GENERAL INFORMATION:
 ; APPLICANT: Loring, Jeanne F.
 ; ATTORNEY: Tingley, Debora W.
 ; APPLICANT: Edwards, Carla M.
 ; ATTORNEY: Streeter, David G.
 ; TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION 1-LIKE PROTEINS
 ; FILE REFERENCE: PC-0013 US
 ; CURRENT APPLICATION NUMBER: US/09/614,474
 ; CURRENT FILING DATE: 2000-07-11
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PERL program
 ; SEQ ID NO: 2
 ; LENGTH: 255
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. 6524819 247500.5
 ; NAME/KEY: unsure
 ; LOCATION: 11
 ; OTHER INFORMATION: unknown or other
 ; US-09-614-474-2

Query Match 59.2%; Score 620.5; DB 4; Length 255;
 Best Local Similarity 62.4%; Pred. No. 2.5e-63;
 Matches 121; Conservative 22; Mismatches 42; Indels 9; Gaps 2;

Qy 5 DLQDPLSATIACHLDPRVFVDGLCRAKFPESLFRTYDKDTTFQYFSFKRVINFSNPLSA 64
 Db 63 DFNDLPLNSLPACNVHQSVFEGESEKSFKEGLFRTYDDCVTFQLFKSFRVRINFSNPKSA 122

Qy 65 ADARLRLHKTEFLGKEMKLKPQTLISPPASPPWQKVQEDATPVINYDLIYASKLGPGEKYELHAA 120
 Db 123 ARARLHETOFRGKLLKLYFAQVTPETDGLKLLAPQPKQFLISPPASPPWQPI 182

Qy 121 EDATPVINYDLIYASKLGPGEKYELHAAQTDPSPVYVHVCESDQEENEEBEMRMRKLP 180
 Db 183 NDATPVINYDLIYAKLGPEKYELHAGTESTSPVVHVCDSDIEEEDPK---TSP 237

Qy 181 KPKI10TRRREYTP 194
 |||||

Db 238 KPKIIQTRRPGLPP 251
RESULT 5
 US-09-949-016-11450
 ; Sequence 11450, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 11450
 ; LENGTH: 206
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-949-016-11450

Query Match 56.9%; Score 596.5; DB 4; Length 192;
 Best Local Similarity 62.2%; Pred. No. 9_8e-61;
 Matches 117; Conservative 21; Mismatches 41; Indels 9; Gaps 2;
 Qy 11 SATIACILDPRVFDGLCRAKFFSLFRITYDKDTTFOYFKSFKRVRINFSNPLSAADARLR 70
 Db 6 STLVACUVDEEVFTNQEVKEFBLFRITYDKDCVTFQLFKSFRRVRINFSNPKSAAARIE 65

Qy 71 LHKTTEFLGKEMKLYFACTLHIGSS---HLAPPNPDKOFLISPPASPVGKQVEDATPV 126
 Db 66 LHETQFRERKCLLYFAQVQTPETDGDKLHLAPPAOKFLISPPSPPVGWFINDATPV 125

Qy 127 INVDLLYAIASKLGPGKELYELHAATDPTPSVWVHVCESDOENEEEMERMRKRPKPKTIQ 186
 Db 126 LNVDLLYAVAKLGPGKELYELHACTESTPSVWVHVCDSIEBEDPK----TSPKPKTIQ 180

Qy 187 TRRBYTP 194
 Db 181 TRRGLPP 188

RESULT 7
 US-09-949-016-6659
 ; Sequence 6659, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SEQ ID NO: 6659
 ; LENGTH: 192
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-949-016-6659

Query Match 56.9%; Score 596.5; DB 4; Length 192;
 Best Local Similarity 62.2%; Pred. No. 9_8e-61;
 Matches 117; Conservative 21; Mismatches 41; Indels 9; Gaps 2;
 Qy 11 SATIACILDPRVFDGLCRAKFFSLFRITYDKDTTFOYFKSFKRVRINFSNPLSAADARLR 70
 Db 6 STLVACUVDEEVFTNQEVKEFBLFRITYDKDCVTFQLFKSFRRVRINFSNPKSAAARIE 65

Qy 71 LHKTTEFLGKEMKLYFACTLHIGSS---HLAPPNPDKOFLISPPASPVGKQVEDATPV 126
 Db 66 LHETQFRERKCLLYFAQVQTPETDGDKLHLAPPAOKFLISPPSPPVGWFINDATPV 125

Qy 127 INVDLLYAIASKLGPGKELYELHAATDPTPSVWVHVCESDOENEEEMERMRKRPKPKTIQ 186
 Db 126 LNVDLLYAVAKLGPGKELYELHACTESTPSVWVHVCDSIEBEDPK----TSPKPKTIQ 180

Qy 187 TRRBYTP 194
 Db 181 TRRGLPP 188

RESULT 8
 US-09-614-474-11
 ; Sequence 11, Application US/09614474
 ; Patent No. 6524819
 ; GENERAL INFORMATION:
 ; APPLICANT: Loring, Jeanne F.

RESULT 6
 US-09-614-474-10
 ; Sequence 10, Application US/09614474
 ; Patent No. 6524819
 ; GENERAL INFORMATION:
 ; APPLICANT: Streeter, David G.
 ; APPLICANT: Tingley, Debra W.
 ; APPLICANT: Edwards, Carla M.
 ; APPLICANT: Edwards, Carla M.
 ; TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION 1-LIKE PROTEINS
 ; FILE REFERENCE: PC-0013 US
 ; CURRENT APPLICATION NUMBER: US/09/614,474
 ; CURRENT FILING DATE: 2000-07-11
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PERL Program
 ; SEQ ID NO: 10
 ; LENGTH: 192
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. 6524819 g1435040
 US-09-614-474-10

APPLICANT: Tingley, Debora W.
 APPLICANT: Edwards, Carla M.
 APPLICANT: Streeter, David G.
 TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION 1-LIKE PROTEINS
 FILE REFERENCE: PC-0013 US
 CURRENT APPLICATION NUMBER: US/09/614,474
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: PERL Program
 SEQ ID NO: 11
 LENGTH: 241
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc Feature
 OTHER INFORMATION: Incyte ID No. 6524819 96017919
 US-09-614-474-11

Query Match Score 56.9%; Score 596; DB 4; Length 241;
 Best Local Similarity 61.9%; Pred. No. 1.6e-60; Indels 10; Gaps 2;
 Matches 120; Conservative 20; Mismatches 44; Indels 10; Gaps 2;

Qy 2 EEVVLQDIPSATIACHLDPRVFDGLCRAKFESLFRITYDKOTTFQYFKSFKVRVRFNSNP 61
 Db 38 EMWDLQDIPSATIACHLDPRVFDGLCRAKFESLFRITYDKOTTFQYFKSFKVRVRFNSKP 97

Qy 62 LSAADARLRHKTEFLGKEMLYFAQTIHIG---SSHLLAPNPDKOFLISPLPASPPVGW 117
 Db 98 EAARARARERELHEIDENGQKLKLYFAQYQMSGEVRDKSYLLPQPKOFLISPLPASPPVGW 157

Qy 11.8 KOVEDATPVINYDLYAISKLGFGEKYLHAAATDPTPSVVVHVCESDQENEREEEMERM 177
 Db 15.8 KOSEDAMPVINYDLYAISKLGFGEKYLHAAATDPTPSVVVHVCESDQENEREEEMERM 177
 Qy .178 KRPKPKLIIQTRRPE 191
 Db 21.2 KNPKQKIAQTRRPPD 225

RESULT 9
 US-09-949-016-7081
 Sequence 7081, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION
 ; APPLICANT: VENNER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CUC01307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0
 ; SEQ ID NO: 7081
 ; LENGTH: 248
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-949-016-7081

Query Match Score 56.9%; Score 596; DB 4; Length 248;
 Best Local Similarity 61.9%; Pred. No. 1.6e-60; Indels 10; Gaps 2;
 Matches 120; Conservative 20; Mismatches 44; Indels 10; Gaps 2;

Qy 2 EEVVLQDIPSATIACHLDPRVFDGLCRAKFESLFRITYDKOTTFQYFKSFKVRVRFNSNP 61
 Db 45 EMWDLQDIPSATIACHLDPRVFDGLCRAKFESLFRITYDKOTTFQYFKSFKVRVRFNSKP 104
 Qy 62 LSAADARLRHKTEFLGKEMLYFAQTIHIG---SSHLLAPNPDKOFLISPLPASPPVGW 117

Db 105 EAAARARARIELHEIDENGQKLKLYFAQYQMSGEVRDKSYLLPQPKOFLISPLPASPPVGW 164
 Qy 118 KOVEDATPVINYDLYAISKLGFGEKYLHAAATDPTPSVVVHVCESDQENEREEEMERM 177
 Db 165 KOSEDAMPVINYDLYAISKLGFGEKYLHAAATDPTPSVVVHVCESDQENEREEEMERM 177
 Qy 178 KRPKPKLIIQTRRPE 191
 Db 219 KNPKQKIAQTRRPPD 232

RESULT 10
 US-09-513-999C-5849
 ; Sequence 5849, Application US/09513999C
 ; Patent No. 6783961
 ; GENERAL INFORMATION:
 ; APPLICANT: Duclert, A.
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 ; Patent No. 6783961
 ; FILE REFERENCE: 59.US2. REG
 ; CURRENT APPLICATION NUMBER: US/09/513,999C
 ; CURRENT FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/122,487
 ; NUMBER OF SEQ ID NOS: 36681
 ; SOFTWARE: Patent .pm
 ; SEQ ID NO: 5849
 ; LENGTH: 111
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-513-999C-5849

Query Match Score 41.9%; Score 439; DB 4;
 Best Local Similarity 84.2%; Pred. No. 7.2e-43;
 Matches 85; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 11 SATIACHLDPRVFDGLCRAKFESLFRITYDKOTTFQYFKSFKVRVRFNSNPLSAADARLR 70
 Db 11 SSSLACVANSDFSESETRAKFESLFRITYDKOTTFQYFKSFKVRVRFNSNPLSAADARLR 70

Qy 71 LHKTTEFLGKEMLYFAQTIHIGSSHLLAPNPDKOFLISPPA 111
 Db 71 LHKTTEFLGKEMLYFAQTIHIGSSHLLAPNPDKOFLISPPA 111

RESULT 11
 US-09-270-767-44503
 ; Sequence 44503, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 44503
 ; LENGTH: 289
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-09-270-767-44503

Query Match Score 35.5%; Score 372.5; DB 4;
 Best Local Similarity 43.8%; Pred. No. 1.4e-34;
 Matches 71; Conservative 38; Mismatches 48; Indels 5; Gaps 3;

Qy 3 EVD--LQDLSATIACHLDPRVFDGLCRAKFESLFRITYDKOTTFQYFKSFKVRVRFNSNP 61
 Db 111 EVDADSDFLPTSIIVNIHSEFANPELKHAMELFRTFSEAFQWLRSFRRLRVNYD 170

Qy 60 NPLSAADARLRLHTEFGLKE-MKLYFAOTL-HIGSSHLAPPNPDQFLISPPASPPVGW 117
 Db 171 NAIANANARIKLHQYEENFKTKVTITCYPAOPVTPVSNKRLQPPAVPKQLISPPASPPAGW 230
 Qy 118 KQVEDATPVINYDLYAISKLGPEBKYLHLAAATDPTPSVYHV 159
 Db 231 SPREEGEPLNHDLAAALASLTPGSHELHPQSEDQPAIIVH 272

RESULT 12
 US-09-854-133-425
 ; Sequence 425, Application US/09854133
 ; GENERAL INFORMATION:
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Mohamath, Raodoh
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Benson, Darin R.
 ; INVENTION: COMPOSITIONS AND METHODS FOR
 ; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.4/P10
 ; CURRENT APPLICATION NUMBER: US/09/854,133
 ; CURRENT FILING DATE: 2001-05-11
 ; NUMBER OF SEQ ID NOS: 735
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 425
 ; LENGTH: 4019
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-854-133-425

Query Match 8.6%; Score 90 5; DB 4; Length 4019;
 Best Local Similarity 27.9%; Pred. No. 2.8%;
 Matches 31; Conservative 15; Mismatches 46; Indels 19; Gaps 4;

Qy 87 QTLHIGSSHLLAPPNPDQFLISPPASPPVG-WKQVEDATPVINYDLYAISKLGGE 142
 Db 935 QVFSPGSNSRSPPSMPDDYAKMGTPRPPVGHSFSRNSAARVENCPPLSSYR---- 989
 Qy 143 KYELHAATDPTPSVYHVCESDQNEEEBEMERMKRKPXPKTIQTRRBYT 193
 Db 990 PLQNETTANRPSPTVDRCLSSSTNND-----PYAKPDPTRPVMT 1030

Query Match 8.6%; Score 90 5; DB 4; Length 4019;
 Best Local Similarity 27.9%; Pred. No. 2.8%;
 Matches 31; Conservative 15; Mismatches 46; Indels 19; Gaps 4;

Qy 87 QTLHIGSSHLLAPPNPDQFLISPPASPPVG-WKQVEDATPVINYDLYAISKLGGE 142
 Db 935 QVFSPGSNSRSPPSMPDDYAKMGTPRPPVGHSFSRNSAARVENCPPLSSYR---- 989
 Qy 143 KYELHAATDPTPSVYHVCESDQNEEEBEMERMKRKPXPKTIQTRRBYT 193
 Db 990 PLQNETTANRPSPTVDRCLSSSTNND-----PYAKPDPTRPVMT 1030

RESULT 13
 PCY-US94-09752-4
 ; Sequence 4, Application PC/TUSS9409752
 ; GENERAL INFORMATION:
 ; APPLICANT: David S. Strayer and Avinash Chander
 ; TITLE OF INVENTION: Compositions and Methods for
 ; TITLE OF INVENTION: Targeting Cells and Modulating Pulmonary Surfactant Secretion
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jane Massey Licata, Esq.
 ; STREET: 210 Lake Drive East, Suite 201
 ; CITY: Cherry Hill
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08002
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
 ; MEDIUM: STORAGE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: WORDPERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/09752
 ; FILING DATE: Herewich
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/176,218

Qy 150 TDPTPSVYHVCESDQNEEEBEMERMKRKPXPKI----IQTRRPEYTP 194
 Db 750 RDPT----RLTRGEEDDEDEGGVIMMRKEPKSPGTDVFTPAPMYS 793

; FILING DATE: December 30, 1993
 ; PRIOR APPLICATION DATA: 08/114,951
 ; APPLICATION NUMBER: 08/114,951
 ; FILING DATE: August 31, 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jane Massey Licata
 ; REGISTRATION NUMBER: 32,257
 ; REFERENCE DOCKET NUMBER: JEFF-0042
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (609) 779-2400
 ; TELEFAX: (609) 779-8488
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 284
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; PCT-US94-09752-4

Query Match 8.4%; Score 88; DB 5; Length 284;
 Best Local Similarity 24.1%; Pred. No. 0.11%;
 Matches 40; Conservative 24; Mismatches 62; Indels 40; Gaps 7;

Qy 27 LCPRAKFEELRYDQDTTFQYFKSFKRVRINFSNPLSADARLRLHKTFLGKEMKLYFA 86
 Db 3 MCYGMMSLFRSGSRQTLFA-----SQMRYAD---LYASFIN--LLYYP 43

Qy 87 QTLHIGSSHLLAPPN-----DKOFLISPPAS---PPVGKQVEDATPVINYDLYA 135
 Db 44 FSYLFRAAHVLMMPHESTVBTHTHDINENESPATRNTSVDFKD---TDYKRHQLTRS 99

Qy 136 SKLGPGKELYLAATDPTPSVYHVCESDQNEEEBEMERMKRPK 181
 Db 100 SETKPNNUFLP-----AQPETHCHEDDDEEEEEECECGKPK 139

RESULT 14
 US-09-824-734-3
 ; Sequence 3, Application US/09824734
 ; Patent No. 6727408

GENERAL INFORMATION:
 ; APPLICANT: ZHU, JIAN-KANG
 ; APPLICANT: SHI, HUAZHONG
 ; APPLICANT: ISHTITANI, MANABU
 ; APPLICANT: STEVENSON, BECKY
 ; TITLE OF INVENTION: PROTEINS AND DNA RELATED TO SALT TOLERANCE IN PLANTS
 ; FILE REFERENCE: 2056440US20
 ; CURRENT APPLICATION NUMBER: US/09/824,734
 ; CURRENT FILING DATE: 2001-04-04
 ; PRIOR APPLICATION NUMBER: US 60/194, 648
 ; PRIOR FILING DATE: 2000-04-04
 ; NUMBER OF SEQ ID NOS: 20
 ; SEQ ID NO: 3
 ; SOFTWARE: PatentIn version 3.1
 ; LENGTH: 822
 ; TYPE: PRT
 ; ORGANISM: Cricetulus griseus
 US-09-824-734-3

Query Match 8.3%; Score 86.5; DB 4; Length 822;
 Best Local Similarity 23.7%; Pred. No. 0.79%;
 Matches 40; Conservative 26; Mismatches 64; Indels 39; Gaps 8;

Qy 44 TFOYFKSPQRVINFSNPLSAA--DARLRLHKTFLGKEMKLYFAQTLH----- 90
 Db 646 TRQLRSYRHTL-VADPYEEAWNQMLRQRQARQLEOKMSNYLTVAHKLDSPMSR 704

Qy 91 IGSHLA-PNPDKQFLISPPASPPVGKQVEDATPVINYDLYAISKGPGEKYELHAA 149
 Db 705 IGSDPLAYEPKADLPVITDPS-----QSPASVDLVNEELKARV-----LGVN 749

Qy 150 TDPTPSVYHVCESDQNEEEBEMERMKRKPXPKI----IQTRRPEYTP 194
 Db 750 RDPT----RLTRGEEDDEDEGGVIMMRKEPKSPGTDVFTPAPMYS 793

RESULT 15
 US-09-575-580b-4.rai
 Sequence 28, Application US/09641741
 Patent No. 6420155
 GENERAL INFORMATION:
 APPLICANT: Kerry E. Quinn
 APPLICANT: Curagen Corporation
 TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids
 TITLE OF INVENTION: encoding Same
 FILE REFERENCE: 15966-81
 CURRENT APPLICATION NUMBER: US/09/641,741
 CURRENT FILING DATE: 2000-08-18
 PRIOR FILING DATE: 1999-10-14
 PRIOR APPLICATION NUMBER: 60/175,534
 PRIOR FILING DATE: 2000-01-12
 PRIOR APPLICATION NUMBER: 60/224,086
 PRIOR FILING DATE: 2000-08-09
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 28
 LENGTH: 719
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-641-741-28

Query Match Score 84.5; DB 4; Length 719;
 Best Local Similarity 21.8%; Pred. No. 1.1;
 Matches 31; Conservative 27; Mismatches 37; Indels 47; Gaps 7;
 Matches 31; Conservative 27; Mismatches 37; Indels 47; Gaps 7;
 Qy 54 VRINFSNLSAADARLRIKTER--LQKEMLYFAQILHICSSHLAPNPDKFLISPP 1.10
 Db 585 LRDPSRMPTPQQRMQRQLQYRLRMEQML--RLNNSDAGPATSTP---ALMPP 637
 Qy 111 ASP-----PVGMK--QVEDATPVINYDLYAISKLGPGEKYELHAATDPT 153
 Db 638 PSPTPAIDLRLPWEVLPTTAGWEESETETVVT-----EFETEYGD-- 681
 Qy 154 PSVYVHYCSDQNEEEFEEFEE 175
 Db 682 ---LEVEEIEEEEEESEBEMD 699

Search completed: November 16, 2005, 16:31:56
 Job time : 29 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: November 16, 2005, 16:22:57 ; Search time 100.8 Seconds
 (without alignments)
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 821.876 Million cell updates/sec

Title: US-09-575-580B-4

Perfect score: 1048

Sequence: 1 MEEVDLQDLPSATIACHLDP.....RPKEKIIQTRRPEVTPHLS 198

Scoring table: BLOSUM62

Gapopen 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters:

1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Published Applications AA:*

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19: /cggn2_6_ptodata/1/pubpaas/US11A_PUBCOMB.pep:*

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21: /cggn2_6_ptodata/1/pubpaas/US60_NEW_PUB.pep:*

22: /cggn2_6_ptodata/1/pubpaas/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1048	100.0	198	9 US-09-782-953-3	Sequence 3, Appli
2	1048	100.0	198	9 US-09-782-953-4	Sequence 4, Appli
3	1009.5	95.7	197	9 US-09-782-953-15	Sequence 15, Appli
4	1009.5	95.7	197	9 US-09-782-953-16	Sequence 16, Appli
5	1002.5	95.7	197	16 US-10-755-889-120	Sequence 120, Appli
6	1002.5	95.7	252	15 US-10-104-7-2892	Sequence 2892, Appli
7	920.5	87.8	198	9 US-09-782-953-6	Sequence 6, Appli
8	920.5	87.8	198	9 US-09-782-953-7	Sequence 7, Appli
9	877.5	83.3	197	9 US-09-782-953-12	Sequence 12, Appli
10	877.5	83.3	197	9 US-09-782-953-13	Sequence 13, Appli
11	872.5	83.3	197	14 US-10-247-671-174	Sequence 174, Appli

12	847.5	80.9	171	15 US-10-428-487-24	Sequence 24, Appli
13	620.5	59.2	243	15 US-10-0-04-2216	Sequence 2216, Appli
14	620.5	59.2	255	14 US-1-0-0-43-2	Sequence 2, Appli
15	613.5	58.5	197	9 US-19-782-953-9	Sequence 9, Appli
16	613.5	58.5	197	9 US-09-782-953-10	Sequence 10, Appli
17	599.5	56.9	192	9 US-09-782-953-18	Sequence 18, Appli
18	596.5	56.9	192	9 US-09-782-953-19	Sequence 19, Appli
19	596.5	56.9	192	14 US-10-290-428-10	Sequence 10, Appli
20	596.5	56.9	197	18 US-10-164-425-126	Sequence 116, Appli
21	596	56.9	241	9 US-09-782-953-21	Sequence 21, Appli
22	596	56.9	241	9 US-09-782-953-22	Sequence 22, Appli
23	596	56.9	241	14 US-10-290-418-11	Sequence 11, Appli
24	595	56.8	212	9 US-09-782-953-24	Sequence 24, Appli
25	595	56.8	212	9 US-09-782-953-25	Sequence 25, Appli
26	497	47.4	142	9 US-09-925-302-790	Sequence 790, Appli
27	497	47.4	142	10 US-09-925-302-790	Sequence 790, Appli
28	379.5	36.7	227	20 US-11-0-143-411-93	Sequence 41193, A
29	284	27.1	58	9 US-09-854-761-35379	Sequence 35379, A
30	284	27.1	58	9 US-09-864-761-43076	Sequence 43076, A
31	271.5	25.9	56	9 US-09-864-761-34111	Sequence 34111, A
32	136.5	13.0	32	14 US-10-194-155-8	Sequence 8, Appli
33	94	9.0	699	16 US-10-437-963-185586	Sequence 185586,
34	93	8.9	227	16 US-10-337-963-196664	Sequence 196664,
35	92	8.8	513	15 US-10-882-122A-46629	Sequence 46629, A
36	92	8.8	1455	18 US-10-511-658-114	Sequence 114, Appli
37	90.5	8.6	4019	9 US-09-738-973-425	Sequence 425, Appli
38	90.5	8.6	4019	9 US-09-854-131-425	Sequence 425, Appli
39	90.5	8.6	4019	14 US-10-144-649-425	Sequence 425, Appli
40	89.5	8.5	915	15 US-10-276-774-2443	Sequence 2443, Appli
41	87.5	8.5	1477	20 US-11-0-97-143-12672	Sequence 12672, A
42	86.5	8.3	822	9 US-09-824-734-2	Sequence 3, Appli
43	86.5	8.3	822	16 US-10-749-963-132441	Sequence 132441,
44	86	8.2	915	16 US-10-437-963-132441	Sequence 132441,
45	85	8.1	2816	15 US-10-240-145-145	Sequence 145, Appli

ALIGNMENTS

RESULT 1	US-09-782-953-3	Sequence 3, Application US-09782953
		; Patent No. US20020150953A1
		; GENERAL INFORMATION:
		; APPLICANT: ROTHERMEL, BEVERLY
		; TITLE OF INVENTION: CALCIURIN INTERACTING PROTEIN (MCIP)
		; FILE REFERENCE: US7SD:674PZ1
		; CURRENT FILING DATE: 2001-02-13
		; PRIORITY APPLICATION NUMBER: US/09/782, 953
		; NUMBER OF SEQ ID NOS: 27
		; SEQ ID NO: 3
		; LENGTH: 198
		; TYPE: PRT
		; ORGANISM: Mus musculus
		US-09-782-953-3

Qy 121 EDATPVINYDLIYAIKGPGKELYELHATDPTPSVYHYCESDOEEREMEMKRP 180
 Db 121 EDATPVINYDLIYAIKGPGKELYELHATDPTPSVYHYCESDOEEREMEMKRP 180

Qy 181 KPKIIQTRPEYTPHLS 198
 Db 181 KPKIIQTRPEYTPHLS 198

RESULT 2
 US-09-782-953-4
 ; Sequence 4, Application US/09782953
 ; Patent No. US20020150953A1
 ; GENERAL INFORMATION
 ; APPLICANT: WILLIAMS, R. SANDERS
 ; APPLICANT: ROTHERMEL, BEVERLY
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
 ; TITLE OF INVENTION: CALCIANEURIN INTERACTING PROTEIN (MCIP)
 ; FILE REFERENCE: USID:674PZ1
 ; CURRENT APPLICATION NUMBER: US/09/782.953
 ; CURRENT FILING DATE: 2001-02-13
 ; PRIOR APPLICATION NUMBER: 60/216,601
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4

Query Match 100.0%; Score 1048; DB 9; Length 198;
 Best Local Similarity 100.0%; Pred. No. 9.e-97; Indels 0; Gaps 0;
 Matches 198; Conservative 0; Mismatches 0;

Db 1 MEEVDIQLPSATIACHILDPRVFDGICRAKESLFRYDQFYSFKRVRINFSN 60
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 Db 61 PLSAADARLRLHKTTEFLGKEMLYFAQLHIGSSHLAPNPDKQFLISPPSPVWQV 120

Qy 121 EDATPVINYDLIYAIKGPGKELYELHATDPTPSVYHYCESDOEEREMEMKRP 180
 Db 121 EDATPVINYDLIYAIKGPGKELYELHATDPTPSVYHYCESDOEEREMEMKRP 180

Qy 181 KPKIIQTRPEYTPHLS 198
 Db 181 KPKIIQTRPEYTPHLS 198

RESULT 3
 US-09-782-953-15
 ; Sequence 15, Application US/09782953
 ; Patent No. US20020150953A1
 ; GENERAL INFORMATION
 ; APPLICANT: WILLIAMS, R. SANDERS
 ; APPLICANT: ROTHERMEL, BEVERLY
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
 ; TITLE OF INVENTION: CALCIANEURIN INTERACTING PROTEIN (MCIP)
 ; FILE REFERENCE: USID:674PZ1
 ; CURRENT FILING DATE: 2001-02-13
 ; PRIOR APPLICATION NUMBER: 60/216,601
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 15

Query Match 100.0%; Score 1048; DB 9; Length 198;
 Best Local Similarity 96.5%; Pred. No. 3.6e-92; Indels 3; Gaps 1;
 Matches 191; Conservative 3; Mismatches 3;

Db 1 MEEVDIQLPSATIACHILDPRVFDGICRAKESLFRYDQFYSFKRVRINFSN 60
 1 MEEVDIQLPSATIACHILDPRVFDGICRAKESLFRYDQFYSFKRVRINFSN 60

Qy 61 PLSAADARLRLHKTTEFLGKEMLYFAQLHIGSSHLAPNPDKQFLISPPSPVWQV 120
 Db 61 PLSAADARLRLHKTTEFLGKEMLYFAQLHIGSSHLAPNPDKQFLISPPSPVWQV 120

Qy 121 EDATPVINYDLIYAIKGPGKELYELHATDPTPSVYHYCESDOEEREMEMKRP 180
 Db 121 EDATPVINYDLIYAIKGPGKELYELHATDPTPSVYHYCESDOEEREMEMKRP 180

Qy 181 KPKIIQTRPEYTPHLS 198
 Db 180 KPKIIQTRPEYTPHLS 197

RESULT 4
 US-09-782-953-16
 ; Sequence 16, Application US/09782953
 ; Patent No. US20020150953A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WILLIAMS, R. SANDERS
 ; APPLICANT: ROTHERMEL, BEVERLY
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
 ; TITLE OF INVENTION: CALCIANEURIN INTERACTING PROTEIN (MCIP)
 ; FILE REFERENCE: USID:74PZ1
 ; CURRENT APPLICATION NUMBER: US/09/782,953
 ; CURRENT FILING DATE: 2001-02-13
 ; PRIOR APPLICATION NUMBER: 60/216,601
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 16

Query Match 100.0%; Score 1048; DB 9; Length 198;
 Best Local Similarity 96.5%; Pred. No. 3.6e-92; Indels 3; Gaps 1;
 Matches 191; Conservative 3; Mismatches 3;

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 Db 61 PLSAADARLRLHKTTEFLGKEMLYFAQLHIGSSHLAPNPDKQFLISPPSPVWQV 120

Qy 121 EDATPVINYDLIYAIKGPGKELYELHATDPTPSVYHYCESDOEEREMEMKRP 180
 Db 121 EDATPVINYDLIYAIKGPGKELYELHATDPTPSVYHYCESDOEEREMEMKRP 180

Qy 181 KPKIIQTRPEYTPHLS 198
 Db 180 KPKIIQTRPEYTPHLS 197

RESULT 5
 US-10-755-889-120
 ; Sequence 120, Application US/10755889
 ; Publication No. US2004017182A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
 ; TITLE OF INVENTION: PATHWAY

FILE REFERENCE: D0284 NP
 CURRENT APPLICATION NUMBER: US/10/755,989
 PRIOR APPLICATION NUMBER: U.S. 60/440,068
 PRIOR FILING DATE: 2004-01-13
 PRIOR APPLICATION NUMBER: U.S. 60/469,757
 PRIOR FILING DATE: 2003-01-14
 NUMBER OF SEQ ID NOS: 823
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 120
 LENGTH: 197
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-755-889-120

Query Match 95.7%; Score 1002.5; DB 16; Length 197;
 Best Local Similarity 96.5%; Pred. No. 3.e-92; Matches 191; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

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Qy 121 EDATPVINYDLLYAIKGPGKELYELHAATDTPPSVWVHCVESDQENEKEEEEMERNRKP 180
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Qy 181 KPKI1QTRPEYPTIHLs 198
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RESULT 6
 US-10-104-047-2892
 i Sequence 2892, Application US/10104047
 i Publication No. US20030236392A1
 i GENERAL INFORMATION:
 i APPLICANT: HELIX RESEARCH INSTITUTE
 i TITLE OF INVENTION: No. US20030236392Ael full length cDNA
 i FILE REFERENCE: H1-A105
 i CURRENT APPLICATION NUMBER: US/10/104.047
 i CURRENT FILING DATE: 2002-03-25
 i PRIOR APPLICATION NUMBER:
 i PRIOR FILING DATE:
 i NUMBER OF SEQ ID NOS: 4096
 i SEQ ID NO: 2892
 LENGTH: 252
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-104-047-2892

Query Match 95.7%; Score 1002.5; DB 15; Length 252;
 Best Local Similarity 96.5%; Pred. No. 5e-92; Matches 191; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

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Qy 121 EDATPVINYDLLYAIKGPGKELYELHAATDTPPSVWVHCVESDQENEKEEEEMERNRKP 180
 Db 176 EDATPVINYDLLYAIKGPGKELYELHAATDTPPSVWVHCVESDQE-KEEEEMERNRKP 234
 Qy 181 KPKI1QTRPEYPTIHLs 198

RESULT 7
 US-09-782-953-6
 i Sequence 6, Application US/09782953
 i Patent No. US20020150952A1
 i GENERAL INFORMATION:
 i APPLICANT: WILLIAMS, R. SANDERS
 i TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
 i TITLE OF INVENTION: CALINEURIN INTERACTING PROTEIN (MCIP)
 i FILE REFERENCE: US/09782953
 i CURRENT APPLICATION NUMBER: US/09/782,953
 i CURRENT FILING DATE: 2001-02-13
 i PRIOR APPLICATION NUMBER: 60/216,601
 i PRIOR FILING DATE: 2000-07-07
 i NUMBER OF SEQ ID NOS: 27
 i SOFTWARE: PatentIn Ver. 2.1
 i SEQ ID NO: 6
 LENGTH: 198
 TYPE: PRT
 i ORGANISM: Mus musculus
 i US-09-782-953-6

Query Match 87.8%; Score 920.5; DB 9; Length 198;
 Best Local Similarity 89.9%; Pred. No. 6.2e-84; Matches 178; Conservative 5; Mismatches 12; Indels 3; Gaps 1;

Db 235 KPKI1QTRPEYPTIHLs 252

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 Db 61 PLSAADARLRLHKTETFLGKEMLYFAQTTHIGSSHLAPPNPDKQFLISPPVGKQV 120

Qy 61 EDATPVINYDLLYAIKGPGKELYELHAATDTPPSVWVHCVESDQENEKEEEEMERNRKP 180
 Db 121 EDATPVINYDLLYAIKGPGKELYELHAATDTPPSVWVHCVESDQE-KEEEEMERNRKP 180

Qy 181 KPKI1QTRPEYPTIHLs 198
 Db 181 KPKI1QTRPEYPTIHLs 198

RESULT 8
 US-09-782-953-7
 i Sequence 7, Application US/09782953
 i Patent No. US20020150952A1
 i GENERAL INFORMATION:
 i APPLICANT: WILLIAMS, R. SANDERS
 i TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
 i TITLE OF INVENTION: CALINEURIN INTERACTING PROTEIN (MCIP)
 i FILE REFERENCE: US/09782953
 i CURRENT APPLICATION NUMBER: US/09/782,953
 i CURRENT FILING DATE: 2001-02-13
 i PRIOR APPLICATION NUMBER: 60/216,601
 i PRIOR FILING DATE: 2000-07-07
 i NUMBER OF SEQ ID NOS: 27
 i SOFTWARE: PatentIn Ver. 2.1
 i SEQ ID NO: 7
 LENGTH: 198
 TYPE: PRT
 i ORGANISM: Mus musculus
 i US-09-782-953-7

Query Match 87.8%; Score 920.5; DB 9; Length 198;
 Best Local Similarity 89.9%; Pred. No. 6.2e-84; Matches 178; Conservative 5; Mismatches 12; Indels 3; Gaps 1;

Qy 4 VDLQDLP---SATIACHILDPRVFDGLCRAKFPESLFRYDKDTTOFYKSFKRVRINFSN 60
 Db 1 MDPRDFSYNSFLSACVNDVFSSETRAKFSLFRYDKDTTOFYKSFKRVRINFSN 60
 ; PRIORITY FILING DATE: 2000-07-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-782-953-13

Qy 61 LLSAADAARLRLHKTFLGKEMKLYFAQTLHIGSSHLAPNPDKQFLISPPASPPVGKQV 120
 Db 61 LLSAADAARLRLHKTFLGKEMKLYFAQTLHIGSSHLAPNPDKQFLISPPASPPVGKQV 120
 ; PRIORITY FILING DATE: 2000-07-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-782-953-13

Qy 121 EDATPVINYDLLIAISKPGKERYELHAATDTPPSVVHVCESDQENECEEEMERNKR 180
 Db 121 EDATPVINYDLLIAISKPGKERYELHAATDTPPSVVHVCESDQENECEEEMERNKR 180
 ; PRIORITY FILING DATE: 2001-07-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 12
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-782-953-13

RESULT 9
 ; Sequence 12, Application US/09782953
 ; Patent No. US2002010953A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WILLIAMS, R. SANDERS
 ; APPLICANT: ROTHERMEL, BEVERLY
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
 ; TITLE OF INVENTION: CALCINERIN INTERACTING PROTEIN (MCIP)
 ; FILE REFERENCE: US7416674
 ; CURRENT APPLICATION NUMBER: US/09/782,953
 ; CURRENT FILING DATE: 2001-07-07
 ; PRIOR APPLICATION NUMBER: 60/216,601
 ; PRIOR FILING DATE: 2000-07-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 12
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-782-953-12

Qy 11 SATIACHILDPRVFDGLCRAKFPESLFRYDKDTTOFYKSFKRVRINFSNPLSAADARL 70
 Db 11 SSILACVANSDFSESETRAKFSLFRYDKDTTOFYKSFKRVRINFSNPLSAADARLQ 70
 ; PRIORITY FILING DATE: 2000-07-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-782-953-13

Qy 71 LHKTBEFLGKEMKLYFAQTLHIGSSHLAPNPDKQFLISPPASPPVGKQVEDATPVINYD 130
 Db 71 LHKTBEFLGKEMKLYFAQTLHIGSSHLAPNPDKQFLISPPASPPVGKQVEDATPVINYD 130
 ; PRIORITY FILING DATE: 2000-07-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-782-953-13

Qy 131 LLYAISKPGKERYELHAATDTPPSVVHVCESDQENECEEEMERNKRPKIIQTRP 190
 Db 131 LLYAISKPGKERYELHAATDTPPSVVHVCESDQENECEEEMERNRPKIIQTRP 189
 ; PRIORITY FILING DATE: 2001-07-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 12
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-782-953-13

RESULT 10
 ; Sequence 13, Application US/09782953
 ; Patent No. US2002010953A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WILLIAMS, R. SANDERS
 ; APPLICANT: ROTHERMEL, BEVERLY
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
 ; FILE REFERENCE: US7416674
 ; CURRENT APPLICATION NUMBER: US/09/782,953
 ; CURRENT FILING DATE: 2001-07-07
 ; PRIOR APPLICATION NUMBER: 60/216,601
 ; PRIORITY FILING DATE: 2000-07-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-782-953-13

Qy 71 LHKTBEFLGKEMKLYFAQTLHIGSSHLAPNPDKQFLISPPASPPVGKQVEDATPVINYD 130
 Db 71 LHKTBEFLGKEMKLYFAQTLHIGSSHLAPNPDKQFLISPPASPPVGKQVEDATPVINYD 130
 ; PRIORITY FILING DATE: 2000-07-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-782-953-13

Qy 131 LLYAISKPGKERYELHAATDTPPSVVHVCESDQENECEEEMERNKRPKIIQTRP 190
 Db 131 LLYAISKPGKERYELHAATDTPPSVVHVCESDQENECEEEMERNRPKIIQTRP 189
 ; PRIORITY FILING DATE: 2001-07-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 12
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-782-953-13

Qy 191 EYTPHILS 198
 Db 190 EYTPHILS 198
 ; PRIORITY FILING DATE: 2000-07-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-782-953-13

RESULT 11
 ; Sequence 14, Application US/10247671
 ; Publication No. US20030194721A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mikita, Thomas
 ; APPLICANT: Shiffman, David
 ; APPLICANT: Porter, Gordon, J.
 ; APPLICANT: Kaser, Matthew R.
 ; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
 ; FILE REFERENCE: PA-0050 US
 ; CURRENT APPLICATION NUMBER: US/10/247,671
 ; CURRENT FILING DATE: 2002-09-18
 ; PRIOR APPLICATION NUMBER: 60/323,784
 ; PRIORITY FILING DATE: 2001-09-19
 ; NUMBER OF SEQ ID NOS: 186
 ; SOFTWARE: PERL, Program
 ; SEQ ID NO 174
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE: misc_feature
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID NO. US20030194721A1 55118B9CD1
 US-10-247-671-174

Qy 11 SATIACHILDPRVFDGLCRAKFPESLFRYDKDTTOFYKSFKRVRINFSNPLSAADARL 70
 Db 11 SSILACVANSDFSESETRAKFSLFRYDKDTTOFYKSFKRVRINFSNPLSAADARLQ 70
 ; PRIORITY FILING DATE: 2000-07-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-247-671-174

Qy 131 LLYAISKPGKERYELHAATDTPPSVVHVCESDQENECEEEMERNKRPKIIQTRP 190
 Db 131 LLYAISKPGKERYELHAATDTPPSVVHVCESDQENECEEEMERNRPKIIQTRP 189
 ; PRIORITY FILING DATE: 2001-07-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-247-671-174

Qy 191 EYTPHILS 198
 Db 190 EYTPHILS 198
 ; PRIORITY FILING DATE: 2000-07-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-247-671-174

RESULT 12
 ; Sequence 15, Application US/10247671
 ; Publication No. US20030194721A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WILLIAMS, R. SANDERS
 ; APPLICANT: ROTHERMEL, BEVERLY
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
 ; FILE REFERENCE: US7416674
 ; CURRENT APPLICATION NUMBER: 60/216,601
 ; CURRENT FILING DATE: 2001-07-07
 ; PRIOR APPLICATION NUMBER: 60/216,601
 ; PRIORITY FILING DATE: 2000-07-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-247-671-174

Qy 131 LLYAISKPGKERYELHAATDTPPSVVHVCESDQENECEEEMERNKRPKIIQTRP 190
 Db 131 LLYAISKPGKERYELHAATDTPPSVVHVCESDQENECEEEMERNRPKIIQTRP 189
 ; PRIORITY FILING DATE: 2001-07-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-247-671-174

Qy 191 EYTPHILS 198
 Db 190 EYTPHILS 198
 ; PRIORITY FILING DATE: 2000-07-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-247-671-174

RESULT 12
US-10-428-487-24
Sequence 24, Application US/10428487
GENERAL INFORMATION:
APPLICANT: GERBER, HANS-PETER
TITLE OF INVENTION: VEGF-MODULATED GENES AND METHODS EMPLOYING THEM
FILE REFERENCE: 09800080-0103
CURRENT APPLICATION NUMBER: US/10/428,487
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: 09/815,153
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,201
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 24
LENGTH: 171
TYPE: PRT
ORGANISM: Homo sapiens
US-10-428-487-24

Query Match Score 847.5; DB 15; Length 171;
Best Local Similarity 95.9%; Pred. No. 1.1e-76;
Matches 162; Conservative 3; N mismatches 3; Indels 1; Gaps 1;

Db 30 AKPESLFRYTDKDTFQYFKSFKRVINFSNPLSADARLRLAKTEFLGKEMLYPAQL 89
Db 4 AKPESLFRYTDKDTFQYFKSFKRVINFSNPLSADARLQLHTEFLGKEMLYPAQL 63
Qy 90 HIGSSHLLAPNPDKOFIISPASPVGKQVEDATPVINYDLIAYAISKGPGKEXELAA 149
Db 64 HIGSSHLLAPNPDKOFIISPASPVGKQVEDATPVINYDLIAYAISKGPGKEXELAA 123

Qy 150 TDPTPSVWVHVCESQENEEERMRKPKLICITRPEPTPIHL 198
Db 124 TDPTPSVWVHVCESDQE-KBEEEEMRMRPKPKLICITRPEPTPIHL 171

RESULT 13
US-10-104-047-2216
Sequence 2216, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. US20030236392A1 full length cDNA
FILE REFERENCE: HL-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
PRIOR APPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 2216
LENGTH: 243
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-2216

Query Match Score 620.5; DB 15; Length 243;
Best Local Similarity 64.4%; Pred. No. 1e-53;
Matches 121; Conservative 22; Mismatches 42; Indels 9; Gaps 2;

Db 5 DLQDLPSSATACHLDPRVFDGLCRAKESLFRTYDQDTFOFKSFKRVINFSNPLS 64
Db 51 DENDLPNSLFACNVHQSVFEGESEKEPKBGLFRTYDDCTFQLKSFRRVRINFSNPLS 110
Qy 65 ADARLRHKTEFLGKEMLYFAQTLHIGSS---HLAPPNPDKOFIISPASPVGKOV 120

Qy 5 DLQDLPSSATACHLDPRVFDGLCRAKESLFRTYDQDTFOFKSFKRVINFSNPLS 64
Db 63 DENDLPNSLFACNVHQSVFEGESEKEPKBGLFRTYDDCTFQLKSFRRVRINFSNPLS 122

Qy 65 ADARLRHKTEFLGKEMLYFAQTLHIGSS---HLAPPNPDKOFIISPASPVGKOV 120
Db 123 ARARIELHEQFRKCKLHYFAQVQTPETDGDKHLAPQPAKFLISPSSPPVGKOP 182

Qy 121 EDATPVINYDLIAYAISKGPGKEXELAAATDPTPSVWVHVCESDQEENEEERMRKRP 180
Db 183 NDATPVINYDLIAYAISKGPGKEXELAGTESTSVWVHVCDESIEEBEDPK----TSP 237

Qy 181 KPKLIQTRPEPYTP 194
Db 238 KPKLIQTRRPGLPP 251

RESULT 14
US-10-230-438-2
Sequence 2, Application US/10290438
Publication No. US20030186333A1
GENERAL INFORMATION:
APPLICANT: Loring, Jeanne F.
APPLICANT: Tingley, Deborah W.
APPLICANT: Edwards, Carla M.
APPLICANT: Streeter, David G.
TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION 1-LIKE PROTEIN
FILE REFERENCE: PC-0013-ICIP
CURRENT APPLICATION NUMBER: US/10/290,438
CURRENT FILING DATE: 2002-11-06
PRIORITY NUMBER: 09/614,474
PRIORITY NUMBER: 2000-07-11
NUMBER OF SEQ ID NOS: 11
SEQ ID NO: 2
LENGTH: 255
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030186333A1 247500.5
FEATURE:
NAME/KEY: unsure
LOCATION: 11
OTHER INFORMATION: unknown or other
US-10-230-438-2

Query Match Score 620.5; DB 14; Length 255;
Best Local Similarity 62.4%; Pred. No. 1.e-53;
Matches 121; Conservative 22; Mismatches 42; Indels 9; Gaps 2;

Qy 5 DLQDLPSSATACHLDPRVFDGLCRAKESLFRTYDQDTFOFKSFKRVINFSNPLS 64
Db 63 DENDLPNSLFACNVHQSVFEGESEKEPKBGLFRTYDDCTFQLKSFRRVRINFSNPLS 122

Qy 65 ADARLRHKTEFLGKEMLYFAQTLHIGSS---HLAPPNPDKOFIISPASPVGKOV 120
Db 123 ARARIELHEQFRKCKLHYFAQVQTPETDGDKHLAPQPAKFLISPSSPPVGKOP 182

Qy 121 EDATPVINYDLIAYAISKGPGKEXELAAATDPTPSVWVHVCESDQEENEEERMRKRP 180
Db 183 NDATPVINYDLIAYAISKGPGKEXELAGTESTSVWVHVCDESIEEBEDPK----TSP 237

Qy 181 KPKLIQTRPEPYTP 194
Db 238 KPKLIQTRRPGLPP 251

RESULT 15
US-09-782-953-9
Sequence 9, Application US/09782953
Patent No. US20020150953A1
GENERAL INFORMATION:
APPLICANT: ROTHERMEL, BEVERLY
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
TITLE OF INVENTION: CALCIUREIN INTERACTING PROTEIN (MCIP)
FILE REFERENCES: UTSD:674PZ1

```

; CURRENT APPLICATION NUMBER: US/09/782,953
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 9
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-782-953-9

Query Match      58.5%; Score 613.5;-DB 9; Length 197;
Best Local Similarity 63.3%; Pred. No. 4e-53; 9; Gaps 2;
Matches 119; Conservative 22; Mismatches 38; Indels 9; Gaps 2;

Qy   11 SATIACHLDPRVYFDGLCRAKEESLFRYDQTKFSKVRINFSNPLSAADARLR 70
Db   11 STLVACVVDVEVFNTNOETEKFEGLFRTYDECYTFOLPKSFRRVINFSHPKSAARARIE 70

Qy   71 LHKTBFLEGEMKLPAQTHIGSS---HLAPNPNDKOFLLSPASPVGQVEDATPV 126
Db   71 LHETOFRGKCKLKYFAQTPTEDGDKLHLAPQPAKFLISPPSPVGWPISDATPV 130

Qy   127 INFDLLYAIASKLGEGEKGELHAATDTPSVVWHVCESDQENEEERERMGRPKPKIQQ 186
Db   131 INFDLLYAVAKLGEGERTELHAGTESTPSVWVCDSDMEEEDPK----TSPKPKLIQ 185

Qy   187 TRPEYTP 194
Db   186 TRRGLPP 193

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Search completed: November 16, 2005, 16:53:28
 Job time : 101.8 secs

GenCore version 5.1.6
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Om protein - protein search, using sw model

Run on: November 16, 2005, 16:43:46 ; Search time 12.15 Seconds
(without alignments)
1567.977 Million cell updates/sec

Title: US-09-575-580B-4
Perfect score: 1048
Sequence: 1 MEEVDQDLSATACHLDP.....RPKKLIQTRRPEYTPHLS 198

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 Summaries

Database : PIR_79:*

- 1: pir1:*
- 2: pir2:*
- 3: pir3:*
- 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	355	33.9	239	2 T34305	hypothetical prote
2	139.5	13.3	315	2 T49641	nebula related pro
3	95.5	9.1	163	2 S62444	conserved hypothet
4	94	9.0	318	2 C84651	hypothetical prote
5	92	8.8	992	2 T46337	hypothetical prote
6	91.5	8.7	1274	2 D84485	probable retrolein
7	88	8.4	284	2 B48516	surfactant protein
8	88	8.4	630	2 S29756	hypothetical prote
9	88	8.4	721	2 S2975	hypothetical prote
10	86.5	8.3	822	2 S30198	Na+/H+ -exchanging
11	86	8.2	338	2 S73902	UDF-Glucose 4-epim
12	84.5	8.1	719	2 S51739	transcription repr
13	83	7.9	561	2 JC2436	5'-nucleotidase (E
14	83	7.9	1173	2 T31421	C-terminal domain-
15	82	7.8	697	2 B96752	hypothetical prote
16	82	7.8	1479	2 T13797	tumor suppressor pr
17	81.5	7.8	528	2 C69323	conserved hypothet
18	81	7.7	151	2 T10768	latex allergen Hev
19	80.5	7.7	280	2 C64471	hypothetical prote
20	80.5	7.7	360	2 S12850	protein TPX - Ther
21	80	7.6	681	2 T17342	hypothetical prote
22	79.5	7.6	797	2 A7053	glutamate ammonia
23	79.5	7.6	904	2 I38757	homolog of Drosoph
24	79.5	7.6	926	2 T29156	homolog of Drosoph
25	79.5	7.6	1020	2 B86414	hypothetical prote
26	79.5	7.6	1136	2 T26553	hypothetical prote
27	79.5	7.6	1146	2 C83104	hypothetical prote
28	79.5	7.6	1557	2 T29132	hypothetical prote
29	7.5	684	2 F85075	hypothetical prote	

RESULT 1

T34305

hypothetical protein F54E7 7 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C;Accession: T34105

R;Bentley, D.

A;Description: The sequence of C. elegans cosmid F54E7.

A;Reference number: 221502

A;Status: Preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Accession: T34105

A;Cross-references: UNIPROT: P53806; EMBL: U00067; PIDN: AAC77519.1; GSPDB: GN00021; CESP: F

A;Experimental source: strain Bristol N2; clone F54E7

C;Genetics:

A;Gene: CESP; F54E7.7

A;Map position: 3

A;Introns: 40/3; 78/2; 165/2; 205/1

Query	Match	Best Local Similarity	Score	DB 2;
Matches	75;	Conservative	33.9%;	No. 3..9e-24;
Qy	8	DIPSATIACHLDPRVFDGLKRAFKESLPLRTYDKDITPQQFPKSFKRVRINFSNPSAADA	67	
Db	27	DLPNAIIYTQVPEDFDNMQDKANFSSLIFTQIEKDIDFELRSRRVTFVSEPPENATAA	86	
Qy	68	RLRHKTEFLGKEMKLKYFAQTLLHI--GSSHILAPPNPDKOFLISPASPSPVGWQVEDATP	125	
Db	87	KLIVQGFSFKGHBLKAFAQRIMYMSANSQMLSPPLEQFLISPCCSPVGMEQTQDNPP	146	
Qy	126	VI-NYDILYAISLKGPGKELYHAATDPTPSVYVYCSDQENEEBEMERMKRPKEPKI	184	
Db	147	VVCFNFDIMARLASPAIDAEKEYINGDETDPAITHPCSTPID-VPSAITEMPTPRSSPS	205	

RESULT 2

T4941

nebulia related protein [Imported] - Neurospora crassa

N;Alternate names: protein B5O22, 230

C;Species: Neurospora crassa

C;Accession: T46641

R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Hartmann, B.; Holland, R.; Nyakatura

submitted to the Protein Sequence Database, May 2000

A;Reference number: 225022

A;Accession: T49641
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-315 <SCH>
A;Cross-references: UNIPROT:Q9PSS9; EMBL:AL355932; GSPDB:GN00116; NCSP:B5O22.230
A;Experimental source: BAC clone B5O22; strain OR74A
C;Genetics:
A;Gene: NCSP:B5O22.230
A;Map position: 6

Query Match 13.3%; Score 139.5; DB 2; Length 315;
Best Local Similarity 40.2%; Pred. No. 7.6e-05;
Matches 39; Conservative 13; Mismatches 38; Indels 7; Gaps 3;

Qy 49 KSPQRVTRNFSNPUSAADARLRLHKTETLGKEMKLYPAQTTLIGSS---HIAAPPNDKQ 104
Db 101 KSPRRIITTFEDBOAIAAVRSWTDGEALIGCRVYQQPTPFDVSAAKHLAPDAGKL 160

Qy 105 FLISPPASPPVGWQ-VEDA--TPVINDLILYAIISKL 138
Db 161 FFISPPASPPVGWMEQRMEDAPNTMVAEDELAELAKL 197

RESULT 4
C84651 hypothetical protein At2g25670 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 @text_change 09-Jul-2004
C;Accession: C84651
R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shua, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
Euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84651
A;Molecule type: DNA
A;Residues: 1-318 <SNTG>
A;Cross-references: UNIPROT:Q9SL96; GB:AE002093; NID:94874305; PIDN:AAD31367.1; GSPDB:GT

C;Genetics:
A;Gene: AT2g25670
A;Map position: 2

Query Match 9.0%; Score 94; DB 2; Length 318;
Best Local Similarity 25.2%; Pred. No. 0.84;
Matches 38; Conservative 19; Mismatches 64; Indels 30; Gaps 5;

Qy 54 VRINFSNPLSADARLRLHKTETLGKEMKLYPAQTTLIGSS---HIAAPPNDKQ 111
Db 13 ITIQTSTNLFAALDTTRKKKSDKAHSK-----GSKSRSREPEKEPEPVYWAFTP 62

Qy 112 SPPVGWQVEDATPVINYDILYAIISKLGPGEKYELHAATDPTPSVYHVCSDDQ3---- 166
Db 63 LKVKGSHADIDDDDDYATATPPGWSMTSLPSH----TDSRVHVBESSESEDILD 117

Qy 167 ----NEEEPEEMERMKRKPCKIQTTRPE 191
Db 118 EGDDDVVEEQETEVQVHPBEPV--KKAPE 146

RESULT 5
T46337 hypothetical protein DKFZp434Q2413.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 @text_change 09-Jul-2004
C;Accession: T46337
R;Koehler, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23037
A;Accession: T46337
A;Molecule type: mRNA
A;Residues: 1-163 <Odb>
A;Cross-references: EMBL:267757; PID:91061288; PID:CAA91769.1; PID:91061292
R;Odell, C.; Bowman, S.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V.
submitted to the EMBL Data Library, November 1995
A;Reference number: S62546
A;Accession: S62549
A;Molecule type: DNA
A;Residues: 1-163 <Odb>
A;Cross-references: EMBL:267757; PID:91061288; PID:CAA91769.1; PID:91061292
R;Odell, C.; Bowman, S.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z21734
A;Accession: T37650
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-163 <Odb>
A;Cross-references: EMBL:254308; PID:CAA91108.1; GSPDB:GN00066; SPDB:SPAC13G6..15C
A;Experimental source: strain 972h-; cosmid c13G6
R;Odell, C.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z21786
A;Accession: T38331
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-163 <Odb>
A;Cross-references: EMBL:267757; PID:CAA91769.1; GSPDB:GN00066; SPDB:SPAC24B11..04C
A;Experimental source: strain 972h-; cosmid c24B11
C;Genetics:
A;Gene: SPAC24B11..04C; SPAC13G6 15C; SPAC24B11..04C
A;Map position: 1L
C;Superposition: Fission yeast hypothetical protein SPAC13G6..15C

Query Match 9.1%; Score 95.5; DB 2; Length 163;
Best Local Similarity 32.1%; Pred. No. 0.27;
Matches 25; Conservative 17; Mismatches 25; Indels 11; Gaps 4;

Qy 96 LAPPNPDQFLISPPASPPVGWQVEDATP---VINYDLILYAIISKLGPGEKYELHAATDP 152
A;Map position: 1L
C;Superposition: Fission yeast hypothetical protein SPAC24B11..04C
A;Gene: SPAC24B11..04C; SPAC13G6 15C; SPAC24B11..04C
A;Map position: 1L
C;Superposition: Fission yeast hypothetical protein SPAC13G6..15C

Query Match 8.8%; Score 92; DB 2; Length 992;
Best Local Similarity 22.7%; Pred. No. 5.2;
Matches 39; Conservative 18; Mismatches 39; Indels 76; Gaps 7;

Qy 96 LAPPNPDQFLISPPASPPVGWQVEDATP---WKOVEDATPVINYDLYTAIS----- 136
Db 245 LSPPLPHEERAQSPPSLSATEEPPQQPEGOPENWEAE-----LGEDSAASLSLQLSLQR 300

Qy 137 -----KLGPG-----EKYELHAATDPTPSV----- 156

Db	301 EQAPSPPAECKGEQHQSQAEELGPQGEEAEDPEEKVAVSPTPPVSPVVRSTEPVAPPEQ	360	Qy	87 QTHIGSSHLLAPPMP-----DKQFLISPPAS----PPVGWQKQVEDATPVINYDLYAI	135
Qy	157 -----VVHVCESDQENEEEEEEMERMKRPKKIIQTRRPEYTPIH	196	Db	44 FSYLFRAHVLMPESTVEHTHYDINENESPATNRNTSVDFPDX---TDYKRHQLRTSI	99
Db	361 LSEALKAMEEAQVLKDODQRHLLESSK-EKMQQLRKLCQEBBBBEFLRLH	411	Qy	136 SKLGPGEKEYLHADTDPPLPSVVFHVCESDQENEEEEEEMERMKRPK 181	
RESULT 6					
Db	D84485	probable retroelement pol polyprotein [imported] - Arabidopsis thaliana	Qy	100 SEIKPPNLFP-----APQEITHCHDEDDDBEEEEECECGSKPK 139	
C;Species:	Arabidopsis thaliana (mouse-eared cress)		Db		
C;Date:	02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004		Qy		
C;Accession:	D84485		Db		
R;Lin., X.; Kaul, S.; Rounslley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayan, L.; Talon, L.; eiss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.			Qy		
A;Title:	Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.		Db		
A;Reference number:	A84420; MUID:20083487; PMID:10617197		Qy		
A;Accession:	D84485		Db		
A;Status:	preliminary		Qy		
A;Molecule type:	DNA		Db		
A;Residues:	1-1274 <STR>		Qy		
A;Cross-references:	UNIPROT:Q9ZQK2; GB:A8002093; PID:94309763; PID:AAD15532;1; GSPDB:GN		Db		
C;Genetics:			Qy		
A;Gene:	At2g07440		Db		
A;Map Position:	2		Qy		
RESULT 8					
Db	S29796	hypothetical protein 2280 - evening primrose chloroplast (fragment)	Qy		
C;Species:	chloroplast Oenothera lamarckiae (evening primrose)		Db		
C;Date:	30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004		Qy		
C;Accession:	S29796		Db		
R;Nimzyk, R.; Schoendorf, T.; Hachtel, W.			Qy		
Curr. Genet.	23, 265-270, 1993		Db		
A;Title:	In-frame length mutations associated with short tandem repeats are located in		Qy		
A;Reference number:	S29795; MUID:93169690; PMID:8435856		Db		
A;Accession:	S29795		Qy		
A;Molecule type:	DNA		Db		
A;Residues:	1-630 <NIN>		Qy		
A;Cross-references:	UNIPROT:P31569; EMBL:X64615; PID:g14331; PID:g14332		Db		
C;Genetics:			Qy		
A;Genome:	chloroplast		Db		
C;Keywords:	chloroplast		Qy		
RESULT 8					
Query	Match	Score 88; DB 2; Length 630;	Query	Match	Score 88; DB 2; Length 630;
Best Local Similarity	23.7%	Pred. No. 7.8;	Best Local Similarity	26.2%	Pred. No. 6.7;
Matches	51;	Mismatches 30;	Matches	23;	Mismatches 48;
Conservative		Indels 51;	Conservative		Indels 56;
		Gaps 9;			Gaps 10;
Qy	24 VDGICRAKEPSLFRPTYDQDTFQVFKSFKVRINFNSNPUSAADAR-LFLHKTEFLGKE--	80	Qy	16 CHLDPRVFDLICRAKEPSLFRPTYDQDTFQVFKSFKVRINFNSNPUSAADARLRLHK 73	
Db	673 IESRVEAKPFGRFESTIENDV----KQKEQLKAIDKSSSYIRDMDNLAKTOPOQTQDN	727	Db	81 CSIDPISIVYIKNLCEAGDSSLYKWKY----FELGTSMKKLT-	118
Qy	81 MKLYFACTLHI---GSSHLLAPPNPD-----KQFLISPPA---SPPVGWK 118		Qy	74 TEFLGKEMKLHYAQTLHIGS---SHLAPPNPDPQFLISPPASPPVGWQVEDATPVINYD 130	
Db	728 PKVQTOQQPDPVKPTNNOPATPEPPSKQADYGKKEITLNELIQKPGGRGRKPSSQPK 787		Db	119 -----LLYLTCSAGSIAQDLLSPPGPDEQNLT----SYGLVEN---DSD 157	
Qy	119 QVEDATPVINYDLYIAISKLGPEKYLH----ATDPPTPSVVFVAVCSDQENESEE 173		Qy	131 LIYAIISKLGPGKEXYLHABA---TDPPTPSVVFVAVCSDQENESEE---EEIME 175	
Db	788 KVSPPTMPKL-----TICKLKLPQSREAKRAEEDSDWVWVTDKVYSEXYNMPLPESDDEE	841	Db	158 LVHGSDIVHG-LLELGALVGSSPTBEVEGTEEVEGTEEVEGTBEVE 208	
Qy	174 MERMKRPKPKLIIQTRR-----PEYTPHILS 198		Qy		
Db	842 TERLUKSVKBIRLKTVKLAPDGRSLINPAMPTHTS 876		Db		
RESULT 9					
Query	Match	Score 88; DB 2; Length 721;	Query	Match	Score 88; DB 2; Length 721;
Best Local Similarity	26.2%	Pred. No. 7.9;	Best Local Similarity	26.2%	Pred. No. 7.9;
Matches	45;	Mismatches 23;	Matches	45;	Mismatches 48;
Conservative		Indels 56;	Conservative		Indels 56;
		Gaps 10;			Gaps 10;
Qy	16 CHLDPRVFDLICRAKEPSLFRPTYDQDTFQVFKSFKVRINFNSNPUSAADARLRLHK 73		Qy	16 CHLDPRVFDLICRAKEPSLFRPTYDQDTFQVFKSFKVRINFNSNPUSAADARLRLHK 73	
Db	81 CSIDPISIVYIKNLCEAGDSSLYKWKY----FELGTSMKKLT-		Db	81 CSIDPISIVYIKNLCEAGDSSLYKWKY----FELGTSMKKLT-	118
Qy	74 TEFLGKEMKLHYAQTLHIGS---SHLAPPNPDPQFLISPPASPPVGWQVEDATPVINYD 130		Qy	74 TEFLGKEMKLHYAQTLHIGS---SHLAPPNPDPQFLISPPASPPVGWQVEDATPVINYD 130	
Db	119 -----LLYLTCSAGSIAQDLLSPPGPDEQNLT----SYGLVEN---DSD 157		Db	119 -----LLYLTCSAGSIAQDLLSPPGPDEQNLT----SYGLVEN---DSD 157	
RESULT 7					
B48516	Surfactant protein A receptor - pig				
C;Species:	Sus scrofa domestica (domestic pig)				
C;Date:	07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 07-Apr-1994				
C;Accession:	B48516				
R;Strayer, D.S.; Yang, S.; Jerng, H.H.					
J. Biol. Chem.	268, 18679-18684, 1993				
A;Title:	Surfactant protein A-binding Proteins. Characterization and structures.				
A;Reference number:	A4516; MUID:93366778; PMID:8366162				
A;Status:	preliminary; not compared with conceptual translation				
A;Molecule type:	mRNA				
A;Residues:	1-284 <STR>				
A;Cross-references:	GB:L10124				
RESULT 7					
Query	Match	Score 88; DB 2; Length 284;	Query	Match	Score 88; DB 2; Length 721;
Best Local Similarity	24.1%	Pred. No. 2.5;	Best Local Similarity	24.1%	Pred. No. 7.9;
Matches	40;	Mismatches 24;	Matches	40;	Mismatches 23;
Conservative		Indels 40;	Conservative		Indels 56;
		Gaps 7;			Gaps 10;
Qy	27 LCRAKFEISLFRTYDQDTFQVFKSFKVRINFNSNPUSAADARLRLHKTEFLGKEMKLHYA 86		Qy	16 CHLDPRVFDLICRAKEPSLFRPTYDQDTFQVFKSFKVRINFNSNPUSAADARLRLHK 73	
Db	3 MCYGMGSLRSGSRQTLFA-----SOVMRYAD---LYAASFN-- 43		Db	81 CSIDPISIVYIKNLCEAGDSSLYKWKY----FELGTSMKKLT-	118

Qy 45 FOYFKSFKVRVRFNSNPLSAADARLRLHKTTEFLGKEMMLYFAQTLHIGSSHLAPPNP--- 101
 Pw 45.0 FA :|: .
 Qy 102 ----DKQFLISPPAS---PPVGWQKVQEDATPVINYDLYAISKLGPGEKYELHAATDPT 153
 Db 491 EHTHDVINEMESPLATRNTSVDPKD---TDYKRHQULTRSISSIKKPMLFPL----A 540
 Qy 154 PSVYVHVCCSDQNEEEEEE 175
 Db 541 PQEITH-CHDEDDDEEEEEE 561

RESULT 14
 T31421 C-terminal domain-binding protein rα1 - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T31421
 R;Turvey, A.; Patturajan, M.; Litingtontung, Y.; Joshi, R.V.; Gentile, C.; Gebara, M.; Cord
 Proc. Natl. Acad. Sci. U.S.A. 93, 6975-6980, 1996
 A;Title: The C-terminal domain of the largest subunit of RNA polymerase II interacts with
 A;Reference number: Z21024; MUID: 8692929
 A;Accession: T31421
 A;Status: Preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-1173 <YTR>
 A;Cross-references: UNIPROT:Q63624; EMBL:U49056; PID:91438532; PIDN: AAC526
 A;Experimental source: hippocampus

Query Match 7.9%; Score 83; DB 2; Length 1173;
 Best Local Similarity 24.1%; Pred. No. 40;
 Matches 49; Conservative 18; Mismatches 88; Indels 48; Gaps 7;

Db 14 VEVVSILDPPDTWPSHLQLQPGSEEDVL--ELVAEVIGDRDPM 56

Qy 1 MEEYDLDQDLPSSATIACHILD---PRVFVDGLCRAKFESLFLRTYDKDTTFQYFKSFKVRVINF 58
 Db 59 SNPLSAADARLRLHKTTEFLGKEMK-----LYFQTLHIGSSHLAPP-----N 100
 Qy 57 PLPVPSSLPLRRAVRT---GKTVSPQSHASRPACSRHLITLGTDGGAPPAASSGS 113

Query Match 7.8%; Score 82; DB 2; Length 697;
 Best Local Similarity 24.7%; Pred. No. 26;
 Matches 44; Conservative 23; Mismatches 65; Indels 46; Gaps 7;

Db 291 DKDTTNOKENSOETPWSDEKIELPRLSDRETOQTSAAFQQAEEIAKRIAKME-SQKR 348

Qy 83 LYFQTLHIGSSHLAPPNDQFPLISPPASPPGVWQKVQEDATPVINYDLYAIS---KLG 139
 Db 349 LLEMQA-----NLDKQMMFTTYSYRRYISKDVEDAT-----YGFSDALKIG 389

Qy 140 PGERKYLELHAATDPPTPSVYVHVVCSD-----QENEEREEPEMERMKRKPCKKIIQTREPEY 192
 Db 390 EGGRGPVTKAVLQYTSVAIKLKGITBGLKQFQQEIEVLSSNRHPNNVILLGACPEY 447

Search completed: November 16, 2005, 17:13:06
 Job time : 14.15 secs

RESULT 15
 E96752 Hypothetical protein F28P22.5 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Accession: E96752
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 R;Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, N.A.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Matiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.B.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venet, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosomes 1 of the Plant Arabidopsis
 A;Reference number: A86141; MUID: 101619; PMID: 11130712
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-697 <STO>

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Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6						
OM protein - protein search, using SW model							
Run on:	November 16, 2005, 16:32:05 ; Search time 49.5 Seconds (without alignment)						
Title:	US-09-575-580B-4						
Perfect score:	1048						
Sequence:	1 MEVDQDLPSSATIACHLDP.....RPKPKLIQTRRPEYTPHLS 198						
Scoring table:	BLOSUM62						
	Gapop 10.0 , Gapext 0.5						
Searched:	1612378 seqs, 512079187 residues						
Total number of hits satisfying chosen parameters:	1612378						
Minimum DB seq length: 0							
Maximum DB seq length: 2000000000							
Post-processing: Minimum Match 0%							
	Maximum Match 100%						
	Listing first 45 summaries						
Database :	UniProt_03: 1: uniprot_sprot:/* 2: uniprot_trembl:/*						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	%						
SUMMARIES							
Result No.	Score	Query	Match	Length	DB	ID	Description
1	1040	99.2	198	1	CCP1_MOUSE	Q91hg6	mus musculus
2	1040	99.2	251	2	QTNTF3_HUMAN	Q91hg3	mus musculus
3	1002.5	95.7	197	1	CCP1_HUMAN	P53805	homo sapien
4	1002.5	95.7	252	2	OTZ555	Q75555	homo sapien
5	887.5	84.7	199	2	Q8k482_RATTUS_NORV	Q8k482	rattus norvegicus
6	884.5	84.4	197	1	CCP1_CRIGR	Q3847	cricetus
7	883.5	84.3	197	2	Q6XXM7_OVIS_ARIES	Q6XXM7	ovis aries
8	883.5	84.3	199	2	Q6IN33_RATTUS_NORV	Q6IN33	rattus norvegicus
9	847.5	80.9	242	2	Q62NM3_HOMO_SAPIEN	Q62NM3	homo sapien
10	834.5	79.6	231	2	Q7ZXP4_XENOPUS_LAEV	Q7ZXP4	xenopus laevis
11	784.5	74.9	199	2	Q6dk90_XENOPUS_TROPOPHORE	Q6dk90	xenopus laevis
12	777.5	74.2	199	2	Q7T0U1_XENOPUS_LAEV	Q7T0U1	xenopus laevis
13	643.5	61.4	210	2	Q6DGB1_BRACHYDANIO	Q6DGB1	brachydanio rerio
14	639.5	61.0	210	2	Q6DC33_BRACHYDANIO	Q6DC33	brachydanio rerio
15	627.5	59.9	243	2	Q8V1P4_MUS_MUSCULUS	Q8V1P4	mus musculus
16	622.5	59.4	243	2	Q8zh26_RATTUS_NORV	Q8zh26	rattus norvegicus
17	618.5	59.0	230	2	Q6D339_BRACHYDANIO	Q6D339	brachydanio rerio
18	613.5	58.5	197	1	CCP2_MOUSE	Q9hg2	mus musculus
19	609.5	58.2	225	2	Q86YJ0_HOMO_SAPIEN	Q86YJ0	homo sapien
20	608.5	58.1	192	2	Q8VIP5_MUS_MUSCULUS	Q8VIP5	mus musculus
21	608.5	58.1	197	2	Q8CH27_RATTUS_NORV	Q8CH27	rattus norvegicus
22	607.5	58.0	243	2	Q8N116_HOMO_SAPIEN	Q8N116	homo sapien
23	606.5	57.9	195	2	Q6NSM4_BRACHYDANIO	Q6NSM4	brachydanio rerio
24	597	57.0	239	1	CCP3_MOUSE	Q91kk0	mus musculus
25	596.5	56.9	197	1	CCP2_HUMAN	Q14206	homo sapien
26	595	56.9	241	1	CCP3_HUMAN	Q9ak8	homo sapien
27	379.5	36.2	292	1	SRA_DRONE	Q9az18	drosophila melanogaster
28	351	33.5	207	1	CCPL_CAEEL	Q53806	caenorhabditis elegans
29	155	14.8	29	1	Q9H2A1_HOMO_SAPIEN	Q9H2A1	homo sapien
30	139.5	13.3	315	2	Q9PPS9_NEUROSPORA	Q9PPS9	neurospora crassa
31	115.5	11.0	249	2	Q66P90_CRYPTOCOCCUS	Q66P90	cryptococcus neoformans

ALIGNMENTS

RESULT 1	
CCP1_MOUSE	STANDARD; PRT; 198 AA;
ID	Q91hg6 ; Q91hg5 ; Q9jxk1 ; Q9jxk2 ; Q9jxk3 ;
AC	Q91hg6 ; Q91hg5 ; Q9jxk1 ; Q9jxk2 ; Q9jxk3 ;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DB	Calcipressin 1 (Down syndrome critical region protein 1 homolog)
DB	(Myocyte-enriched calcineurin interacting protein 1) (MCIP1).
GN	Name=Dscr1;
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Buteleostomi; Mammalia; Butcheria; Rodentia; Sciurognathi; Murinae; Mus.
OX	NCBI TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A. (ISOFORM A).
RC	STRAIN=BALB/C; TISSUE=Brain;
RX	MEDLINE=20534792; PubMed=11080588; DOI=10.1101/S0378-1119(00)00407-8;
RA	Strippoli P., Petrini M., Lenzi L., Caronni P., Zannotti M.; RT "The murine DSCR1-like (Down syndrome candidate region 1) gene family: conserved synteny with the human orthologous genes.";
RL	Gene 257:223-232(2000).
RN	[2]
RP	SEQUENCE FROM N.A. (ISOFORMS A AND B).
RX	MEDLINE=1017590; PubMed=1072214; DOI=10.1074/jbc.275.12.8719;
RA	Rothermel B., Vega R.B., Yang J., Wu H., Bassel-Duby R., Williams R.S.; RT "A protein encoded within the Down syndrome critical region is enriched in striated muscles and inhibits calcineurin signaling.";
RA	J. Biol. Chem. 275:8719-8725(2000).
RN	[3]
RP	SEQUENCE FROM N.A. (ISOFORM A), AND FUNCTION.
RC	TISSUE=Fetal brain;
RX	MEDLINE=2115920; PubMed=11231093; DOI=10.1101/S0925-4773(00)00583-9;
RA	Casas C., Martínez S., Pritchard M.A., Fuentes J.J., Nadal M., Gimera J., Arbones M., Flores J., Soriano E., Estivill X., Alcantara S.; RT "Dscr1, a novel endogenous inhibitor of calcineurin signaling, is expressed in the primitive ventricle of the heart and during neurogenesis"; RT Mech. Dev. 101:289-292(2001).
RL	
RP	SEQUENCE FROM N.A. (ISOFORMS B AND C).
RA	Fuentes J.J., Pritchard M.A., Pucharcos C., Estivill X.; RT "Down syndrome candidate region 1 (Dscr1), one of three alternatively spliced exon 1 transcripts"; RT Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN	[4]
RP	SEQUENCE FROM N.A. (ISOFORM C).
RC	STRAIN=C57BL/6J; TISSUE=Embryonic stem cells;
RX	MEDLINE=22334683; PubMed=1246681; DOI=10.1038/nature01266;
RA	Okazaki Y., Furuno M., Kasukawa T.T., Adachi J., Bono H., Kondo S., Niikido I., Osato N., Saito R., Suzuki H., Yamamoto T., Kiyobawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Bradd D., Brusic V., Chobani C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Garibaldi M., Gissi C., Godzik A., Gough J., Grumich S., Gusinovich S., Hirakawa N., Jackson J., Jarvis E.D., Kanai A., Kawaji H., Kawassa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Perete G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultan R., Takehara Y., Taylor M.S., Teasdale R.D., Tonita M., Verardo R., Wagner L., Wahlastedt C., Wells C., Wilming L.G., Wyryshaw Boris A., Yanagisawa M., Yang I., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Komio T., Kawai J., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Waki A., Arizawa K., Fukuda S., Hara A., Hashizume W., Imorani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasada D., Shibusawa K., Shingawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y., RT	SEQUENCE FROM N.A. (ISOFORM B).	RP	DR	CC
RC	TISSUE-Kidney;	RC	DR	DR	DR
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	RX	DR	DR	DR
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner K.H., Schueler G.D., Altshul S.R., Zeiberg B., Buetow K.H., Schaefer C.M., Schueler G.D., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Bhattacharyya S., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Marusina K., Soares M.B., Bonaldo M.F., Brownstein M.J., Usdin T.B., Toshiyuki S., Casavant T.L., Cheeetz T.B., Raha S., Loquellano N.A., Peters G.J., Carninci P., Prange C., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialus D.E., Schnerr A., Schein J.E., Jones S.J.M., Marra M.A., RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";	RT	AC	CC
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)	RT	DT	DT	CC
RL	-!- FUNCTION: Inhibits calcineurin-dependent transcriptional responses by binding to the catalytic domain of calcineurin A. Could play a role during central nervous system development.	RL	DT	DT	CC
CC	-!- ALTERNATIVE PRODUCTS:	CC	DB	DB	CC
CC	Event=Alternative splicing; Named isoforms=3;	CC	GN	OS	CC
CC	Comment=Additional isoforms seem to exist;	CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Name=A; Synonyms=\$;	OC	CC
CC	IsoId-Q9JHG6-1; Sequence=Displayed;	CC	NCBI_TaxID=10090; [1]	RN	CC
CC	IsoId-Q9JHG6-2; Sequence=VSP_001317;	CC	SEQUENCE FROM N.A.	RP	CC
CC	Name=C;	CC	STRATAN-NIH/Swiss-PROT; TISSUE=Heart;	AC	CC
CC	IsoId-Q9JHG6-3; Sequence=VSP_001318;	CC	Medline=2280613; PubMed=12803556; DOI=10.1042/BJ20030267;	DT	CC
CC	-!- TISSUE SPECIFICITY: Highly expressed in heart and skeletal muscle. Also expressed in all other tissues.	CC	Genesca L., Abareda A., Fuentes J.J., Estivill X., de la Luna S., Perez-Riba M.	DT	CC
CC	-!- SIMILARITY: Belongs to the DSCRI family.	CC	"Phosphorylation of calcipressin 1 increases its ability to inhibit calcineurin and decreases calcipressin half-life.";	DT	CC
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC	Biochem. J. 374: 567-575 (2003).	RL	CC
CC	CC	GO:0005737; C:cycloplasm; IDA.	DR	CC	
CC	CC	InterPro: IPR006931; Calcipressin.	DR	CC	
CC	CC	Pfam; PF04847; Calcipressin.	DR	CC	
CC	SEQUENCE 251 AA; 28137 MW; 09F47C73D847FB2B CRC64;	CC	SEQUENCE 251 AA; 28137 MW; 09F47C73D847FB2B CRC64;	SQ	CC

Query	1	MEEVDLQPLSATIACHLDPRVFDGICRAKEFESLFRTYDKDTTFQYFKSPKRVRINFSN	Score 1.040; DB 2; Length 251;
Best Local Similarity	99.2%	Pred. No. 1-2e-80;	
Matches	197;	Conservative 0; Mismatches 1;	Indels 0; Gaps 0;
Db	54	MEEVLDLQPLSATIACHLDPRVFDGICRAKEFESLFRTYDKDTTFQYFKSPKRVRINFSN	SEQUENCE OF 1-164 FROM N.A. (ISOFORM 2).
Qy	61	PLSAAADARLRLHKTKEFLGKEMLYFAQTLHGSSHLAPPNPDKQFLISPLASPPYQWKOY	RA Rodriguez A.C., Grinwood J.J., Schmutz J.J., Myers R.M., Smailus D.E., RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., RA Schein J.E., Jones S.J.M., Marra M.A.; RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). [5]
Db	114	PLSAAADARLRLHKTKEFLGKEMLYFAQTLHGSSHLAPPNPDKQFLISPLASPPYQWKOY	RT SEQUENCE OF 1-164 FROM N.A. (ISOFORM 2).
Qy	121	EDATPVINYDLIYISKLGPEKYLHATAATDTPSVVVHVCSDQNEEEBEMERMKRP	RA Crawford D.R., Leahy K.P., Davies K.J.A.; RT "Adapt78, a calcium and oxidant-inducible RNA.";
Db	174	EDATPVINYDLIYISKLGPEKYLHATAATDTPSVVVHVCSDQNEEEBEMERMKRP	RT Submitted (APR1996) to the EMBL/GenBank/DBJ databases. [6]
Qy	181	KPKIIQTTRPEYPTIHLIS	RA CHARACTERIZATION, RX MEDLINE=20320698; PubMed=10861295; DOI=10.1093/hmg/9.11.1681; RA Fuentes J.J., Genesca L., Kingsbury T.J., Cunningham K.W., Perez-Riba M., Estivill X., de la Luna S.; RT "DSCRL, overexpressed in Down syndrome, is an inhibitor of calcineurin-mediated signaling pathways"; RT Hum. Mol. Genet. 9:1681-1690(2000).
Db	234	KPKIIQTTRPEYPTIHLIS	-1- FUNCTION: Inhibits calcineurin-dependent transcriptional responses by binding to the catalytic domain of calcineurin A. Could play a role during central nervous system development.
Qy	1	HUMAN STANDARD; PRT; 197 AA.	CC -1- ALTERNATIVE PRODUCTS: Named isoforms=4;
AC	P53805;	Q00582; Q00583; Q96R03; Q9BU69; Q9UME4;	CC Event-Alternative splicing; Named isoforms=4;
DT	01-OCT-1996 (Rel. 34; Created)		CC Name=;
DT	16-OCT-2001 (Rel. 40; Last sequence update)		CC IsoID=P53805-1; Sequence=Displayed;
DT	05-JUL-2004 (Rel. 44; Last annotation update)		CC Name=;
DE	Calciressin 1 (Down syndrome critical region protein 1) (Myocyte-enriched calcineurin interacting protein 1) (MCIP1) (adapt78).		CC IsoID=P53805-2; Sequence=VSP_001314;
DE	Name=USCR1; Synonyms=ADAP78, DSC1;		CC Name=;
GN	Homo sapiens (Human)		CC IsoID=P53805-3; Sequence=VSP_001315;
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1]		CC Name=;
OC			CC IsoID=P53805-4; Sequence=VSP_001316;
OC			-1- TISSUE SPECIFICITY: Highly expressed heart, brain and skeletal muscle. Also expressed in all other tissues.
NCBI_TaxID	9606;		CC -1- INDUCTION: By calcium.
PN			CC -1- SIMILARITY: Belongs to the DSCRL family.
RP	SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).		CC
RX	MEDLINE=96121591; PubMed=8595418;		CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RA	Fuentes J.-J., Pritchard M.A., Planas A.M., Bosch A., Ferrer I., Estivill X.;		CC
RT	"A new human gene from the Down syndrome critical region encodes a proline-rich protein highly expressed in fetal brain and heart.",		CC
RT	Hum. Mol. Genet. 4:1935-1944 (1995).		CC
RL	[2]		CC
RN	SEQUENCE FROM N.A., AND ALTERNATIVE SPlicing.		CC
RX	MEDLINE=97468152; PubMed=9325050; DOI=10.1006/geno.1997.4866;		CC
RA	Fuentes J.-J., Pritchard M.A., Estivill X.;		DR EMBL: U28833; AAB81557.1; -.
RT	"Genomic organization, alternative splicing, and expression patterns of the DSCRL (Down syndrome candidate region 1) gene.",		DR EMBL: U85265; AAB84370.1; -.
RT	Genomics 44:358-361(1997).		DR EMBL: U85266; AAB84371.2; -.
RL	[3]		DR EMBL: U85267; AAB84372.1; -.
RN	SEQUENCE FROM N.A. (ISOFORM 3).		DR EMBL: AF400429; AAK92478.1; -.
RA	Hua F., Wu J., Zhou Y., Zhang B., Peng X., Qiang B., Yuan J., Qiang B.;		DR EMBL: BC002864; AAB02864.1; -.
RA	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.		DR EMBL: US5821; AAF21218.1; -.
RN	[4]		DR Gene, HGNC: 3040; DSCR1.
RP	SEQUENCE FROM N.A. (ISOFORM 1).		DR H-InvDB: HIX0016091; -.
RC	TISSUE=Lung;		DR MIM: 602917; -.
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		DR GO; GO:0005634; C:nucleus; TAS.
RA	Strasberg R.L., Reingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schulter G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Mariusina K., Farmer A.A., Rubin G.M., Hong D., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Yoshihii S., Carmincio C., Rahal S.S., Loquaiola N.A., Petters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Soedergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whaling M., Madan A., Young A.C., Sheen E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Bouffard G.G.,	DR GO; GO:0003700; P:transcription factor activity; TAS.	
RA			DR GO; GO:0007417; P:central nervous system development; TAS.
RA			DR GO; GO:0008015; P:circulation; TAS.
RA			DR InterPro; IPR006931; Calcipressin.
RA			DR PF03847; PFam; PF04847; Calcipressin; 1.
RA			KW Alternative splicing.
RA			FT DOMAIN 166 174
RA			FT VARSPLIC 1 28
RA			FT VARSPLIC 1 28
RA			FT VARSPLIC 1 29
RA			FT VARSPLIC 1 80

FT	CONFLICT	147	147	H -> R (in Ref. 3).
FT	SEQUENCE	159	159	H -> Q (in Ref. 5).
SQ	SEQUENCE	197 AA;	22637 MW;	1BD42BBB881676C CRC64;
Query Match	Best Local Similarity	95.7%;	Score 1002.5;	DB 1; Length 197;
Matches 191; Conservative 3; Mismatches 3; Indels 1; Gaps 1;				
Qy	1	MEEVDLQLPSSATIACHLDPRVFDGLCRAKFESLFRYDQTTFQFKSFKRVRINFSN 60		RESULT 5
Db	1	MEEVDLQLPSSATIACHLDPRVFDGLCRAKFESLFRYDQTTFQFKSFKRVRINFSN 60		Q8K4S2 PRELIMINARY; PRT; 199 AA.
Qy	61	PISAAADARLRLHTEFLGKEMLYFAQTLHIGSSHLLAPNPDKQFLISPPASPVGMKQV 120		AC Q8K4S2; PRELIMINARY; PRT; 199 AA.
Db	61	PISAAADARLRLHTEFLGKEMLYFAQTLHIGSSHLLAPNPDKQFLISPPASPVGMKQV 120		AC Q8K4S2; PRELIMINARY; PRT; 199 AA.
Qy	121	EDATPVINYDILYIAISKLGPGEKYLEHAATDTPSPVVHVCESDQEEEMERMKRP 180		DT DT 01-OCT-2002 (TREMBLrel. 22, Created)
Db	121	EDATPVINYDILYIAISKLGPGEKYLEHAATDTPSPVVHVCESDQEEEMERMKRP 179		DT DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
Qy	181	KPKIIQTRPPEPTPIHL 198		DT DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
Db	180	KPKIIQTRPPEPTPIHL 197		DE Myoocyte-enriched calcineurin-interacting protein 1.
Qy	1	MEEVDLQLPSSATIACHLDPRVFDGLCRAKFESLFRYDQTTFQFKSFKRVRINFSN 60		GN Name=mcip_1;
Db	1	MEEVDLQLPSSATIACHLDPRVFDGLCRAKFESLFRYDQTTFQFKSFKRVRINFSN 60		OS Rattus norvegicus (Rat).
Qy	61	PISAAADARLRLHTEFLGKEMLYFAQTLHIGSSHLLAPNPDKQFLISPPASPVGMKQV 120		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Db	61	PISAAADARLRLHTEFLGKEMLYFAQTLHIGSSHLLAPNPDKQFLISPPASPVGMKQV 120		OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Rattus.
Qy	1	MEEVDLQLPSSATIACHLDPRVFDGLCRAKFESLFRYDQTTFQFKSFKRVRINFSN 60		NCBI_TaxID=10116;
Db	1	MEEVDLQLPSSATIACHLDPRVFDGLCRAKFESLFRYDQTTFQFKSFKRVRINFSN 60		[1]
Qy	1	MEEVDLQLPSSATIACHLDPRVFDGLCRAKFESLFRYDQTTFQFKSFKRVRINFSN 60		OS Rattus norvegicus (Rat).
Db	1	MEEVDLQLPSSATIACHLDPRVFDGLCRAKFESLFRYDQTTFQFKSFKRVRINFSN 60		RA Odashima M., Nagata K., Obata K., Somura F., Izawa H., Miyazaki T.,
Qy	61	PISAAADARLRLHTEFLGKEMLYFAQTLHIGSSHLLAPNPDKQFLISPPASPVGMKQV 120		RA Murata Y., Seo H., Yamada Y., Yokota M.,
Db	61	PISAAADARLRLHTEFLGKEMLYFAQTLHIGSSHLLAPNPDKQFLISPPASPVGMKQV 120		RA Murata Y., Seo H., Yamada Y., Yokota M.,
Qy	121	EDATPVINYDILYIAISKLGPGEKYLEHAATDTPSPVVHVCESDQEEEMERMKRP 180		RA Murata Y., Seo H., Yamada Y., Yokota M.,
Db	121	EDATPVINYDILYIAISKLGPGEKYLEHAATDTPSPVVHVCESDQEEEMERMKRP 179		RA Murata Y., Seo H., Yamada Y., Yokota M.,
Qy	181	KPKIIQTRPPEPTPIHL 198		DR Submitted to the EMBL/GenBank/DDJB databases.
Db	180	KPKIIQTRPPEPTPIHL 197		DR EMBL: AB075973; Bac06443_1;
Qy	1	MEEVDLQLPSSATIACHLDPRVFDGLCRAKFESLFRYDQTTFQFKSFKRVRINFSN 60		DR GO:0019722; P:calcium-mediated signaling; IBA.
Db	1	MEEVDLQLPSSATIACHLDPRVFDGLCRAKFESLFRYDQTTFQFKSFKRVRINFSN 60		DR InterPro: IPR006931;
Qy	61	PISAAADARLRLHTEFLGKEMLYFAQTLHIGSSHLLAPNPDKQFLISPPASPVGMKQV 120		DR Pfam: PF04847; Calcipressin_1;
Db	61	PISAAADARLRLHTEFLGKEMLYFAQTLHIGSSHLLAPNPDKQFLISPPASPVGMKQV 120		DR SEQENCE FROM N.A.
Qy	1	MEEVDLQLPSSATIACHLDPRVFDGLCRAKFESLFRYDQTTFQFKSFKRVRINFSN 60		DR Query Match Score 887.5; DB 2; Length 199;
Db	1	MEEVDLQLPSSATIACHLDPRVFDGLCRAKFESLFRYDQTTFQFKSFKRVRINFSN 60		DR Best Local Similarity 91.5%; Fred. No. 9e-68;
Qy	61	PISAAADARLRLHTEFLGKEMLYFAQTLHIGSSHLLAPNPDKQFLISPPASPVGMKQV 120		DR Matches 173; Conservative 3; Mismatches 12; Indels 1; Gaps
Db	61	PISAAADARLRLHTEFLGKEMLYFAQTLHIGSSHLLAPNPDKQFLISPPASPVGMKQV 120		DR Qy 11 SATIACHLDPRVFDGLCRAKFESLFRYDQTTFQFKSFKRVRINFSN 60 AADRLR
Qy	121	EDATPVINYDILYIAISKLGPGEKYLEHAATDTPSPVVHVCESDQEEEMERMKRP 180		DR Qy 11 SLIAVCAVNGDVSSETRAKFESLFRYDQTTFQFKSFKRVRINFSN 60 AADRLR
Db	121	EDATPVINYDILYIAISKLGPGEKYLEHAATDTPSPVVHVCESDQEEEMERMKRP 179		DR Qy 71 LHKTBEFLGKEMLYKAQTLHIGSSHLLAPNPDKQFLISPPASPVGMKQVQEDATPVINYD
Qy	181	KPKIIQTRPPEPTPIHL 198		DR Qy 71 LHKTBEFLGKEMLYKAQTLHIGSSHLLAPNPDKQFLISPPASPVGMKQVQEDATPVINYD
Db	180	KPKIIQTRPPEPTPIHL 197		DR Qy 131 LYAISKLGPGEKYLHAATTTPSPVVHVCESDQEEEMERMKRP KPKIIQTRR
Qy	1	MEEVDLQLPSSATIACHLDPRVFDGLCRAKFESLFRYDQTTFQFKSFKRVRINFSN 60		DR Qy 131 LYAISKLGPGEKYLHAATTTPSPVVHVCESDQEEEMERMKRP KPKIIQTRR
Db	1	MEEVDLQLPSSATIACHLDPRVFDGLCRAKFESLFRYDQTTFQFKSFKRVRINFSN 60		DR SEQUENCE FROM N.A.
Qy	61	PISAAADARLRLHTEFLGKEMLYFAQTLHIGSSHLLAPNPDKQFLISPPASPVGMKQV 120		DR TISSUE=Heart;
Db	61	PISAAADARLRLHTEFLGKEMLYFAQTLHIGSSHLLAPNPDKQFLISPPASPVGMKQV 120		DR MEDLINE=228061131; PubMed=12809556; DOI=10.1042/BJ20030267;
Qy	121	EDATPVINYDILYIAISKLGPGEKYLEHAATDTPSPVVHVCESDQEEEMERMKRP 180		DR RN [1] _;
Db	121	EDATPVINYDILYIAISKLGPGEKYLEHAATDTPSPVVHVCESDQEEEMERMKRP 180		DR Perez-Riba M.;
Qy	181	KPKIIQTRPPEPTPIHL 198		DR "Phosphorylation of calcipressin 1 increases its ability to inhibit
Db	180	KPKIIQTRPPEPTPIHL 197		RT calcineurin and decreases calcipressin half-life.";
Qy	1	MEEVDLQLPSSATIACHLDPRVFDGLCRAKFESLFRYDQTTFQFKSFKRVRINFSN 60		RT Biochem. J. 374:567-575 (2003).
Db	1	MEEVDLQLPSSATIACHLDPRVFDGLCRAKFESLFRYDQTTFQFKSFKRVRINFSN 60		DR EMBL:AY325903; AAP95743_1; -
Qy	61	PISAAADARLRLHTEFLGKEMLYFAQTLHIGSSHLLAPNPDKQFLISPPASPVGMKQV 120		DR GO:0019722; P:calcium-mediated signaling; IBA.
Db	61	PISAAADARLRLHTEFLGKEMLYFAQTLHIGSSHLLAPNPDKQFLISPPASPVGMKQV 120		DR InterPro: IPR006931; Calcipressin.
Qy	121	EDATPVINYDILYIAISKLGPGEKYLEHAATDTPSPVVHVCESDQEEEMERMKRP 180		DR Pfam: PF04847; Calcipressin.
Db	121	EDATPVINYDILYIAISKLGPGEKYLEHAATDTPSPVVHVCESDQEEEMERMKRP 180		DR SEQUENCE FROM N.A.
Qy	181	KPKIIQTRPPEPTPIHL 198		DR MEDLINE=7732995; PubMed=9185508; DOI=10.1006/abbi.1997.0109;
Db	180	KPKIIQTRPPEPTPIHL 197		DR Crawford D.R., Leahy K.P., Abramova N., Lan L., Wang Y., Davies K.J.;
Qy	235	KPKIIQTRPPEPTPIHL 198		DR "Hamster adapt78 RNA is a Down syndrome critical region homologue that is inducible by oxidative stress";
Db	235	KPKIIQTRPPEPTPIHL 252		DR RT Arch. Biochem. Biophys. 342:6-12 (1997).
Qy	1	MEEVDLQLPSSATIACHLDPRVFDGLCRAKFESLFRYDQTTFQFKSFKRVRINFSN 60		CC -- FUNCTION: Inhibits calcineurin-dependent transcriptional response by binding to the catalytic domain of calcineurin A. Could play a role during central nervous system development (By similarity).
Db	1	MEEVDLQLPSSATIACHLDPRVFDGLCRAKFESLFRYDQTTFQFKSFKRVRINFSN 60		CC - INDUCTION: By oxidative stress.
Qy	56	MEEVDLQLPSSATIACHLDPRVFDGLCRAKFESLFRYDQTTFQFKSFKRVRINFSN 115		CC - SIMILARITY: Belongs to the DSC1 family.
Db	56	MEEVDLQLPSSATIACHLDPRVFDGLCRAKFESLFRYDQTTFQFKSFKRVRINFSN 115		CC - INDUCTON: By oxidative stress.
Qy	61	PISAAADARLRLHTEFLGKEMLYFAQTLHIGSSHLLAPNPDKQFLISPPASPVGMKQV 120		CC -
Db	61	PISAAADARLRLHTEFLGKEMLYFAQTLHIGSSHLLAPNPDKQFLISPPASPVGMKQV 120		CC -
Qy	116	PISAAADARLRLHTEFLGKEMLYFAQTLHIGSSHLLAPNPDKQFLISPPASPVGMKQV 175		CC -
Db	116	PISAAADARLRLHTEFLGKEMLYFAQTLHIGSSHLLAPNPDKQFLISPPASPVGMKQV 175		CC -
Qy	121	EDATPVINYDILYIAISKLGPGEKYLEHAATDTPSPVVHVCESDQEEEMERMKRP 180		CC -
Db	121	EDATPVINYDILYIAISKLGPGEKYLEHAATDTPSPVVHVCESDQEEEMERMKRP 180		CC -
Qy	176	EDATPVINYDILYIAISKLGPGEKYLEHAATDTPSPVVHVCESDQEEEMERMKRP 234		CC -
Db	176	EDATPVINYDILYIAISKLGPGEKYLEHAATDTPSPVVHVCESDQEEEMERMKRP 234		CC -


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DR MGD; MGI:1858219; Descr11;
GO; GO:001972; P:calcium-mediated signaling; 1EA.
DR P6am; PRO4847; Calciumpressin; 1.
SQ SEQUENCE 243 AA; 27332 MW; 2CD8C1A810291851 CRC64;

Query Match      59.9%; Score 627.5; DB 2; Length 243;
Best Local Similarity 62.4%; Pred. No. 1.7e-45;
Matches 121; Conservative 24; Mismatches 40; Indels 9; Gaps 2;

Qy   5 DLQDIPSAATTACHLDPRVFDGLCRAKPESLFRYDKOTTFQPKSFRRVNFSNPISA 64
Db   51 DFDSDLPNSLFACNYHQSPFEEEEEKEKPGFLFRYDECVTFOLFKSFRRVRNFSPRSA 110

Qy   65 ADARURLHKTFLGKEMKUYFAQTLHIGSS---HLAPPNPDKOFLISSLPPASPPVGWQKV 120
Db   111 ARARIEELHEFQFRGKKLKLYFAQVOTPTEDGDKLHLAPQPAQQLISPPSSPPVGWQKI 170

Qy   121 EDATPVLINYDLYAISKLGPGEKEYELHAATDPTPSVVVHVCESDQENPEEEEMERMKRP 180
Db   171 SDATPVLINYDLYAVAKLGPGKEYELHAAGTESTPSVVVHCDSDMEBBDPK----TSP 225

Qy   181 KPKLIQTRREPEYTP 194
Db   226 KPKLIQTRRPGLPP 239

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Search completed: November 16, 2005, 17:12:34
 Job time : 52.5 secs

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GenCore version 5.1.6
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Om protein - protein search, using sw model

Run on: November 16, 2005, 16:22:56 ; Search time 125.95 Seconds
(without alignments)
743.120 Million cell updates/sec

Title: US-09-575-580b-5
Perfect score: 1296
Sequence: 1 EFVDPVRPRVRLQOASIP.....TSPPKINQTRPGLPPFGH 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%
Maximum Match 10%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:
1: geneseq1980s:
2: geneseq1990s:
3: geneseq2000s:
4: geneseq2001s:
5: geneseq2002s:
6: geneseq2003s:
7: geneseq2003bs:
8: geneseq2004s:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Aam17859 Peptide #
Abb34672 Peptide #
Abb34677 Peptide #
Aan28174 Peptide #
Aam30365 Peptide #
Abb2995 Peptide #
Abb20081 Protein #
Aam67851 Human bone
Aam57623 Human brain
Aam55464 Human brain
Abg49494 Human liver
Abg51723 Human liver
Aam03406 Peptide #
Aam05506 Peptide #
Abg39657 Human pep
Abg37397 Human pep
Aam14405 Peptide #
Abb33353 Peptide #
Aam26818 Peptide #
Abb28178 Human pep

ALIGNMENTS

RESULT 1
ID AAB31788 standard; protein; 234 AA.
XX
AC AAB31788;
XX
DT 30-APR-2001 (first entry)
XX
DE Amino acid sequence of a human detoxification protein.
XX
KW Human; detoxification protein; DEX; cancer; leukaemia; melanoma;
adenocarcinoma; autoimmune disorder; inflammatory disorder;
rheumatoid arthritis; asthma; atherosclerosis; autoimmune thyroiditis;
psoriasis; ulcerative colitis; infection; cell proliferative disorder;
actinic keratosis; arteriosclerosis; cirrhosis; hepatitis;
KW
XX
OS Homo sapiens.
XX
FH Key
FT Peptide
FT /note= "signal peptide"
1..27
XX
FT Modified-site
FT /note= "potential phosphorylation site"
58
XX
FT Modified-site
FT /note= "potential phosphorylation site"
75
XX
FT Modified-site
FT /note= "potential phosphorylation site"
87
XX
FT Modified-site
FT /note= "potential phosphorylation site"
94
XX
FT Modified-site
FT /note= "potential glycosylation site"
130
XX
FT Modified-site
FT /note= "potential phosphorylation site"
204
XX
FT Modified-site
FT /note= "potential phosphorylation site"
215
XX
FT Modified-site
FT /note= "potential phosphorylation site"
223
XX
FT Modified-site
FT /note= "potential phosphorylation site"
204
XX
PN WO200104305-A2.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1129	87.1	234 4 AAB31788	Aab31788 Amino acid
2	1129	87.1	243 7 ADB64062	Abd64062 Human pro
3	1129	87.1	255 5 AAM50760	Aam50760 Human Dow
4	1129	87.1	255 7 ADE37339	Ad37339 Human Dow
5	882	68.1	197 5 AAE18913	Aae18913 Mouse MCI
6	861	66.4	197 6 ABO07172	Ab007172 Human p53
7	848	65.4	192 5 AAE18916	Aae18916 Human MCI
8	848	65.4	192 7 ADE37341	Ad37341 Human Dow
9	708.5	54.7	241 5 AAE18917	Aae18917 Human MCI
10	708.5	54.7	241 6 ABO07173	Ab007173 Human p53
11	708.5	54.7	241 7 ADE37342	Ad37342 Human Dow
12	676.5	52.2	212 5 AAE18918	Aae18918 Human MCI
13	648	50.0	252 5 ADB64738	Ad64738 Human pro
14	616	47.5	197 5 AAE18915	Aae18915 Human MCI
15	616	47.5	197 5 AAE18914	Aae18914 Human MCI
16	616	47.5	197 7 ADE35770	Ad35770 Human pro
17	616	47.5	197 8 ADR14119	Ad14119 Human NF-
18	613.5	47.3	198 5 AAE18912	Aae18912 Mouse MCI
19	606.5	46.8	198 5 AAE18911	Aae18911 Human MCI
20	582	44.9	242 8 ADR10481	Ad10481 Human pro
21	565	43.6	171 2 AAW73898	Aaw73898 Human Dow
22	418.5	32.3	292 4 ABB71467	Abb71467 Drosophil
23	312	24.1	111 3 AAG01768	Aag01768 Human SEC
24	289	22.3	142 3 AAB58452	Aab58452 Lung cancer
25	213	16.4	58 4 AAM15671	Aam15671 Peptide #

86	SKEFEGLFRTYDDCVTFQFLFKSFRVRINFSNPKSAARARIEHETQFRSKKLKLYFAQ	145	Db	11	STLVACVVDVEFTNQVKFEGLFRTYDECVTQFLFKSFRVRINFSNPKSAARARIE	70
134	VQTPEDGDKLHLAPPQAKOFLISPPSPVGWKPISIDATPVNLTLTAVAKLGPGEK	193	Qy	117	LHETQFRGKKLPLFYEAQVQTPTEDGDKLHLAPPQAKOFLISPPSPVGWKPISIDATPV	176
146	VQTPEDGDKLHLAPPQAKOFLISPPSPVGWKPISIDATPVNLTLTAVAKLGPGEK	205	Db	71	LHETQFRGKKLPLFYEAQVQTPTEDGDKLHLAPPQAKOFLISPPSPVGWKPISIDATPV	130
194	YELHAGTESTPSVWVHVCDSDMEREEDPCKTSKPKINQTRRPGLPP	239	Qy	177	INYDLYAVAKLGPGKYEYLHAGTESTPSVWVHVCDSDMEREEDPCKTSKPKINQTRRPG	236
206	YELHAGTESTPSVWVHVCDSDIEEEEEDPCKTSKPKIQTTRRPGLPP	251	Db	131	INYDLYAVAKLGPGKYEYLHAGTESTPSVWVHVCDSDMEREEDPCKTSKPKIQTTRRPG	190
RESULT 5			Qy	237	LPP 239	
ID	AAE18913	standard	protein; 197 AA.	Db	191	LPP 193
XX	XX	XX				
AC	AAE18913;					
RESULT 6						
			ABO07172	ID	ABO07172 standard; protein; 197 AA.	
			XX	XX		
			AC	ABO07172;		
			XX	XX		
			DT	13-AUG-2003	(first entry)	
			DE	Human p53 modifying protein, SEQ ID 132.		
			XX	XX		
			KW	Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;		
			KW	antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer;		
			KW	lung cancer; ovarian cancer; angiogenesis; cell cycle;		
			KW	apoptotic disorder; cell proliferation disorder.		
			XX	Homosapiens.		
			OS	OS		
			XX	PN	WO200299122-A1.	
			XX	XX		
			PD	12-DEC-2002.		
			XX	XX		
			XX	PF	03-JUN-2002; 2002WO-US017382.	
			XX	PF	05-JUN-2001; 2001US-0295676P.	
			XX	PR	10-OCT-2001; 2001US-0328605P.	
			XX	PR	15-FEB-2002; 2002US-0357253P.	
			XX	XX		
			PA	(EXEL-) EXELIXIS INC.		
			XX	Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;		
			XX	WPI; 2002-179658/23.		
			XX	DR WPI; 2003-156859/15.		
			XX	DR N-PSDB; ACD13348.		
			XX	XX		
			PT	Identifying modulators of the p53 pathway for use in treating apoptotic		
			PT	cell proliferation disorders, comprising screening for agents that		
			PT	modulate activity of a human ortholog of genes that modify the p53		
			PT	pathway in Drosophila.		
			XX	Example 2: Page 434-435; 678pp; English.		
			XX	The invention relates to identifying (M1) a candidate p53 pathway		
			CC	modulating agent, by contacting an assay system comprising a purified HM		
			CC	polypeptide (human orthologue of genes that modify the p53 pathway in		
			CC	Mammalian cell) or nucleic acid with a test agent under conditions where but		
			CC	for the presence of the test agent, the system provides a reference		
			CC	activity, and detecting a test agent-biased activity of the assay system.		
			CC	Also included are modulating (M2) a p53 pathway of a cell comprising		
			CC	contacting a cell defective in p53 function with a candidate modulator		
			CC	that specifically binds to a HM polypeptide comprising an HM amino acid		
			CC	sequence, where p53 function is restored), modulating (M3) a p53 pathway		
			CC	in a mammalian cell (comprising contacting the cell with an agent that		
			CC	specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)		
			CC	a disease in a patient (comprising: (a) obtaining a biological sample		
			CC	from the patient; (b) contacting the sample with a probe for HM pathway		
			CC	expression; (c) comparing the results with a control; and (d) determining		
			CC	whether the comparison indicates a likelihood disease). (M1) is useful		
			CC	Sequence 197 AA;		
			CC	Query Match Score 68.1%; DB 5; Length 197;		
			CC	Best Local Similarity 91.8%; Pred. No. 5.2e-85;		
			CC	Matches 168; Conservative 3; Mismatches 12; Indels 0; Gaps 0;		
			CC	OY		
			CC	57 NSLIFACNVHOSVFEESSEKBFEGLFRTYDBCVTEQFLFKSFRVRINFSNPKSAARARIE 116		

CC for identifying modulators of the p53 pathway. A probe for HM expression
 CC is useful for diagnosing breast, colon, kidney, lung and ovarian cancer.
 CC Modulators identified by (M1) are useful in a variety of diagnostic and
 CC therapeutic applications, where disease or disorder prognosis is related
 CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell
 CC proliferation disorders (e.g., cancer). Another two new methods (M2 and
 CC M3) are useful for modulating the p53 pathway of a cell, thus restoring
 CC the p53 function of the cell, so that the cell undergoes normal
 CC proliferation or progression through the cell cycle. (M2) and (M3) are
 CC also useful for treating defects in the p53 pathway such as angiogenic,
 CC apoptotic or cell proliferation disorders. The present sequence
 CC represents a human p53 pathway modifying protein.

XX
Sequence 197 AA;

Query Match Score 861; DB 6; Length 197;

Best Local Similarity 89.1%; Pred. No. 8.8e-83;
Matches 163; Conservative 8; Mismatches 12; Indels 0; Gaps 0;SQ 57 NSLFACNYHQSVFREEEESKEKFKEGFLFRYDECYTFOFLPKSFRVRINFSHPKSAARARIE 116
DB 11 STLVACVVDVEVFPTNQEVTEKEFKELFLRTYDDCIVTFOFLPKSFRVRINFSNPKSAARARIE 70Qy 117 LHETQFRGKLLKLYFAQVQTPETDGDKLHAPPQAKQLISPPSSPVGWKPISDATPV 176
DB 71 LHETQFRGKLLKLYFAQVQTPETDGDKLHAPPQAKQLISPPSSPVGWQINDATPV 130Qy 177 LNDLILYAVAKLGPGCEKYLHAGTESTPSVWVHVCDSMEREEDPCTSPKPKLNQTRPG 236
DB 131 LNDLILYAVAKLGPGCEKYLHAGTESTPSVWVHVCSDIEBEDPCTSPKPKLNQTRPG 190Qy 237 LPP 239
DB 191 LPP 193RESULT 7
ID AAE18916 standard; protein; 192 AA.

AC AAE18916;

DT 17-MAY-2002 (first entry)

DE Human MCIP associated protein #3.

KW Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy;

KW heart failure; cardiomyopathy; heart disease; human.

OS Homo sapiens.

XX WO200204491-A2.

XX 17-JAN-2002.

XX 06-JUL-2001; 2001WO-US021662.

PP 07-JUL-2000; 2000US-0216601P.

PR 13-FEB-2001; 2001US-00782953.

XX PA (TEXA) UNIV TEXAS SYSTEM.

PA (WILL/) WILLIAMS S. R.

PA (ROTH/) ROTHERMEL B.

PI Williams SR, Rothermel B;

XX DR WPI; 2002-179698/23.

DR N-PSDB; AAD30157.

XX Screening for modulators of muscle calcineurin interacting protein (MCIP)

PR binding, expression or phosphorylation, useful for treating cardiac

PR hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a

CC test compound.

CC Example 1; Page 165-166; 174pp; English.

CC XX PT XX

CC The invention relates to muscle calcineurin interacting proteins (MCIPs).

CC CC The invention relates to muscle calcineurin interacting such proteins. MCIPs form a physical

CC complex with the catalytic subunit of calcineurin and increased levels of

CC MCIPs correspond to a reduced ability of calcineurin to stimulate

CC CC transcription of certain target genes. The invention also relates to

CC CC methods for identifying modulators of MCIP binding, expression or

CC CC phosphorylation. Inhibitors or promoters of MCIP may be used for treating cardiac

CC CC hypertension and heart failure.

CC Antibodies to MCIP can be used in characterising the MCIP content of

CC healthy and diseased tissues and subsequently for determining the

CC presence or absence of cardiomyopathy or as predictor of heart disease.

CC The present sequence is human MCIP associated protein. Note: This

CC sequence has been described as human MCIP splice variant in

CC specification, however the sequence seems to be a MCIP associated protein

XX SQ Sequence 192 AA;

Query Match Score 848; DB 5; Length 192;

Best Local Similarity 88.0%; Pred. No. 2.1e-81;

Matches 161; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

Qy 57 NSLFACNYHQSVFREEEESKEKFKEGFLFRYDECYTFOFLPKSFRVRINFSHPKSAARARIE 116
DB 6 STLVACVVDVEVFPTNQEVTEKEFKELFLRTYDDCIVTFOFLPKSFRVRINFSNPKSAARARIE 65Qy 117 LHETQFRGKLLKLYFAQVQTPETDGDKLHAPPQAKQLISPPSSPVGWKPISDATPV 176
DB 66 LHETQFRGKLLKLYFAQVQTPETDGDKLHAPPQAKQLISPPSSPVGWQINDATPV 125Qy 117 LHETQFRGKLLKLYFAQVQTPETDGDKLHAPPQAKQLISPPSSPVGWKPISDATPV 176
DB 66 LHETQFRGKLLKLYFAQVQTPETDGDKLHAPPQAKQLISPPSSPVGWQINDATPV 125RESULT 8
ADE37341 standard; protein; 192 AA.
ID ADE37341
XX DE ADE37341;
XX AC ADB37341;
XX DT 29-JAN-2004 (first entry)
XX DE Human Down syndrome critical region 1-like 1 protein.
XX KW Down syndrome critical region 1-like 1 alpha protein; nootropic;
KW neuroprotective; peptide therapy; gene therapy; Alzheimer's disease;
KW human; Down syndrome critical region 1-like 1 protein.
XX OS Homo sapiens.

DB 186 LPP 188

Qy 237 LPP 239

DB 126 LNDLILYAVAKLGPGCEKYLHAGTESTPSVWVHVCDSMEREEDPCTSPKPKLNQTRPG 236

Qy 177 LNDLILYAVAKLGPGCEKYLHAGTESTPSVWVHVCDSMEREEDPCTSPKPKLNQTRPG 236

DB 126 LNDLILYAVAKLGPGCEKYLHAGTESTPSVWVHVCDSMEREEDPCTSPKPKLNQTRPG 185

Qy 237 LPP 239

DB 186 LPP 188

RESULT 8
ADE37341 standard; protein; 192 AA.
ID ADE37341
XX DE ADE37341;
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XX DE Human Down syndrome critical region 1-like 1 protein.
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KW human; Down syndrome critical region 1-like 1 protein.
XX OS Homo sapiens.

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Qy 237 LPP 239

DB 126 LNDLILYAVAKLGPGCEKYLHAGTESTPSVWVHVCDSMEREEDPCTSPKPKLNQTRPG 236

Qy 177 LNDLILYAVAKLGPGCEKYLHAGTESTPSVWVHVCDSMEREEDPCTSPKPKLNQTRPG 236

DB 126 LNDLILYAVAKLGPGCEKYLHAGTESTPSVWVHVCDSMEREEDPCTSPKPKLNQTRPG 185

Qy 237 LPP 239

DB 186 LPP 188

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Qy 177 LNDLILYAVAKLGPGCEKYLHAGTESTPSVWVHVCDSMEREEDPCTSPKPKLNQTRPG 236

DB 126 LNDLILYAVAKLGPGCEKYLHAGTESTPSVWVHVCDSMEREEDPCTSPKPKLNQTRPG 185

Qy 237 LPP 239

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XX OS Homo sapiens.

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DB 126 LNDLILYAVAKLGPGCEKYLHAGTESTPSVWVHVCDSMEREEDPCTSPKPKLNQTRPG 236

Qy 177 LNDLILYAVAKLGPGCEKYLHAGTESTPSVWVHVCDSMEREEDPCTSPKPKLNQTRPG 236

DB 126 LNDLILYAVAKLGPGCEKYLHAGTESTPSVWVHVCDSMEREEDPCTSPKPKLNQTRPG 185

Qy 237 LPP 239

DB 186 LPP 188

RESULT 8
ADE37341 standard; protein; 192 AA.
ID ADE37341
XX DE ADE37341;
XX AC ADB37341;
XX DT 29-JAN-2004 (first entry)
XX DE Human Down syndrome critical region 1-like 1 protein.
XX KW Down syndrome critical region 1-like 1 alpha protein; nootropic;
KW neuroprotective; peptide therapy; gene therapy; Alzheimer's disease;
KW human; Down syndrome critical region 1-like 1 protein.
XX OS Homo sapiens.

DB 186 LPP 188

Qy 237 LPP 239

DB 126 LNDLILYAVAKLGPGCEKYLHAGTESTPSVWVHVCDSMEREEDPCTSPKPKLNQTRPG 236

Qy 177 LNDLILYAVAKLGPGCEKYLHAGTESTPSVWVHVCDSMEREEDPCTSPKPKLNQTRPG 236

DB 126 LNDLILYAVAKLGPGCEKYLHAGTESTPSVWVHVCDSMEREEDPCTSPKPKLNQTRPG 185

Qy 237 LPP 239

DB 186 LPP 188

RESULT 8
ADE37341 standard; protein; 192 AA.
ID ADE37341
XX DE ADE37341;
XX AC ADB37341;
XX DT 29-JAN-2004 (first entry)
XX DE Human Down syndrome critical region 1-like 1 protein.
XX KW Down syndrome critical region 1-like 1 alpha protein; nootropic;
KW neuroprotective; peptide therapy; gene therapy; Alzheimer's disease;
KW human; Down syndrome critical region 1-like 1 protein.
XX OS Homo sapiens.

DB 186 LPP 188

Qy 237 LPP 239

DB 126 LNDLILYAVAKLGPGCEKYLHAGTESTPSVWVHVCDSMEREEDPCTSPKPKLNQTRPG 236

Qy 177 LNDLILYAVAKLGPGCEKYLHAGTESTPSVWVHVCDSMEREEDPCTSPKPKLNQTRPG 236

DB 126 LNDLILYAVAKLGPGCEKYLHAGTESTPSVWVHVCDSMEREEDPCTSPKPKLNQTRPG 185

PT diagnosing and treating Alzheimer's disease, and for identifying and purifying antibodies that specific bind to the protein.

PS Disclosure: SEQ ID NO 10; 39pp; English.

XX This invention relates to a novel purified Down syndrome critical region of 255 amino acids, as given in the specification. Compounds which modulate the protein of the invention may have nootropic or neuroprotective activity. The protein sequence of the invention and the cDNA sequence which encodes it may be useful for peptide therapy and gene therapy respectively. The invention may prove useful in development of therapeutics for the treatment of Alzheimer's disease. The present sequence is the amino acid sequence of the human Down syndrome critical region 1-like 1 protein which was used to demonstrate homology to the Down syndrome critical region 1-like 1 alpha protein which was used to determine the invention.

XX Sequence 192 AA;

Query Match 65.4%; Score 84.8; DB 7; Length 192;

Best Local Similarity 88.0%; Pred. No. 2.1e-81; Matches 161; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

Qy 57 NSLIFACNTHQSVPFEEERKEKEFEGLPRTYDECUTFQLFKSFRVRLINSHPKSAARARIE 116

Db 6 STLVACVVDVEVFTNQEVKEKFGKLFLPRTYDDCUTFQLFKSFRVRLINSHPKSAARARIE 65

Qy 117 LHETQFRRKLPYFAQVQTPTEDGDKHHLAPQPAQAKFLISPPSSPSVGWKPISDATPV 176

Db 66 LHETQFRGKKLKLYFAQVQTPTEDGDKHHLAPQPAQFLISPPSSPSVGWKPISDATPV 125

Qy 177 LNYDLILYAVAKLGPGEKXYBLHAGTESTSVVYHVCDSDMEREEDPKTSPEKPKINGOTRRPG 236

Db 126 LNYDLILYAVAKLGPGEKXYBLHAGTESTSVVYHVCDSDMEREEDPKTSPEKPKIICQTRPG 185

Qy 237 LPP 239

Db 186 LPP 188

RESULT 9

ABE18917

ID AAE18917 standard; protein, 241 AA.

XX AAE18917;

XX AC AAE18917;

XX DT 17-MAY-2002 (First entry)

XX DE Human MCIP associated protein #4.

XX KW Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy; heart failure; cardiomyopathy; heart disease; human.

XX OS Homo sapiens.

XX PN WO200204491-A2.

XX PD 17-JAN-2002.

XX PP 06-JUL-2001; 2001WO-US021662.

XX PR 07-JUL-2000; 2000US-0216601P.

XX PR 13-FEB-2001; 2001US-00782933.

XX PA (TEXA) UNIV TEXAS SYSTEM.

PA (WILL/) WILLIAMS S. R.

PA (ROTH/) ROTHERMEL B.

XX PI Williams SR, Rothermehl B;

XX DR WPI; 2002-179698/23.

DR N-PSDB, AAD30158.

XX

PT Screening for modulators of muscle calcineurin interacting protein (MCIP) binding, expression or phosphorylation, useful for treating cardiac hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a test compound.

XX PS Example 1; Page 168-169; 174pp; English.

XX The invention relates to muscle calcineurin interacting proteins (MCIPs) and nucleic acid molecules encoding such proteins. MCIPs form a physical complex with the catalytic subunit of calcineurin and increased levels of MCIPs correspond to a reduced ability of calcineurin to stimulate transcription of certain target genes. The invention also relates to methods for identifying modulators of MCIP binding, expression or phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin may be used for treating cardiac hypertrophy and heart failure.

XX Antibodies to MCIP can be used in characterising the MCIP content of healthy and diseased tissues and subsequently for determining the presence or absence of cardiomyopathy or as predictor of heart disease.

XX The present sequence is human MCIP associated protein. Note: This sequence has been described as splice variant of MCIP initiated by exon 4 in the specification, however the sequence seems to be a MCIP associated protein.

XX Sequence 241 AA;

Query Match 54.7%; Score 708.5; DB 5; Length 241; Best Local Similarity 66.2%; Pred. No. 1.9e-49; Mismatches 3; Gaps 2; Matches 141; Conservative 20; Mismatches 20; Indels 3; Gaps 2;

Qy 28 LCCIDRDWATQCPA-EFAQALTFESDLPNSLACNPHOSVPEEEESKXPEGFLRTY 85

Db 16 LCSTDQEEEEEMIGENEDLDDEMIDLSDLPLTSIFACSVHEAFEARERQERFEALFTIY 75

Qy 86 DECUTFOLFKSFRRVRINFSHPSKSAARARIBLHETOFRGKLPFLYFAQVOTPTEDGDKLH 145

Db 76 DDQVTQLFLKSFRRVRINFSPEAKRARIBLHETDNGQKLIFQAQVOMSGERDKSY 135

Qy 146 LAPPOPAKQFLISPLSPSSPSVWKPIISDATPVNLYAYAKLGPKGEKYELHAGTBTSPS 205

Db 136 LIPQPQPKQFLISPLSPSSPSVWKQSDAMPVINYDILCAVSKLGPKGEKYELHAGTBTSPS 195

Qy 206 VVVHVCDSDMEREEDPKTSPKPKINOTRRPGP 238

Db 196 VVVHVCESETBEEETK-NPQQKIAQTRRPDP 227

RESULT 10

ABO07173

ID ABO07173 standard; protein, 241 AA.

XX AC ABO07173;

XX DT 13-AUG-2003 (First entry)

XX DB Human p53 modifying protein, SBQ ID 133.

XX KW Human; p53 modifier; cyrostatic; cancer; cyrostatic; antiangiogenic;

KW ant apoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle; apoptotic disorder; cell proliferation disorder.

XX Homo sapiens.

XX OS Homo sapiens.

XX PN WO200299122-A1.

XX

XX PD 12-DEC-2002.

XX PR 03-JUN-2002; 2002WO-US017382.

XX

PA	(EXEL-) EXELIXIS INC.	DT 29-JAN-2004 (first entry)
XX	Human Down syndrome critical region 1-like 2 protein.	XX
PI	Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;	DE
XX	WPI: 2003-156859/15.	XX
DR	N-PSDB: ACD13349.	KW
XX	Down syndrome critical region 1-like 1alpha protein; nootropic; neuroprotective; peptide therapy; gene therapy; gene therapy; Alzheimer's disease; human; Down syndrome critical region 1-like 2 protein.	KW
PR	Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53 pathway in Drosophila.	KW
XX	OS Homo sapiens.	XX
PT	US2003186333-A1.	PN
PR	Example 2; Page 435-436; 678pp; English.	XX
PS	Example 2; Page 435-436; 678pp; English.	XX
CC	The invention relates to identifying (M1) a candidate p53 pathway modulating agent, by contacting an assay system comprising a purified HM polypeptide (human ortholog of genes that modify the p53 pathway in Drosophila) or nucleic acid with a test agent under conditions where but for the presence of the test agent, the system provides a reference system, activity, and detecting a test agent biased activity of the assay system.	CC
CC	Also included are modulating (M2) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid sequence, where p53 function is restored), modulating (M3) a p53 pathway in a mammalian cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with probe for HM expression; (c) comparing the results with a control; and (d) determining whether the comparison indicates a likelihood disease). (M1) is useful for identifying modulators of the p53 pathway. A probe for HM expression is useful for diagnosing breast, colon, kidney, lung and ovarian cancer. Modulators identified by (M1) are useful in a variety of diagnostic and therapeutic applications, where disease or disorder prognosis is related to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell proliferation disorders (e.g. cancer). Another two new methods (M2 and M3) are useful for modulating the p53 pathway of a cell, thus restoring the p53 function of the cell, so that the cell undergoes normal proliferation or progression through the cell cycle. (M2) and (M3) are also useful for treating defects in the p53 pathway such as angiogenic, apoptotic or cell proliferation disorders. The present sequence represents a human p53 pathway modifying protein.	CC
CC	Sequence 241 AA;	XX
SQ	Query Match 54.7%; Score 708.5; DB 6; Length 241; Best Local Similarity 66.2%; Pred. No. 1.9e-66; Matches 141; Conservative 20; Mismatches 49; Indels 3; Gaps 2;	Query Match 54.7%; Score 708.5; DB 7; Length 241; Best Local Similarity 66.2%; Pred. No. 1.9e-66; Matches 141; Conservative 20; Mismatches 49; Indels 3; Gaps 2;
Db	28 LCCIDRDAVTOCPA--EBAFOALTDSDLPLNSLFACYHVSFEERSEKEKPEGLPRTY 85	Qy 28 LCCIDRDAVTOCPA--EBAFOALTDSDLPLNSLFACYHVSFEERSEKEKPEGLPRTY 85
Qy	16 LCSTDQEEMEDDLEMDMSLQLTSIPACSHAAFEARQEREAALFTY 75	Db 16 LCSTDQEEMEDDLEMDMSLQLTSIPACSHAAFEARQEREAALFTY 75
Db	86 DECYTFQLFKSFRVRINFSHPKSAAARIELHETQFGKKLPLYFAQVQTPTDGDKH 145	Qy 86 DECYTFQLFKSFRVRINFSHPKSAAARIELHETQFGKKLPLYFAQVQTPTDGDKLH 145
Qy	76 DDQYTFQLPKSFRVRINFSHPKSAAARIELHETDFQKQKLKLYFAQVQMSGEVRDKSY 135	Db 76 DDQYTFQLPKSFRVRINFSHPKSAAARIELHETDFQKQKLKLYFAQVQMSGEVRDKSY 135
Db	146 LAPPQPAKOFPLISPPSSPSVGWKPISDATPVINYDLIYAVAKLGPGKELYHAGTESTPS 205	Qy 146 LAPPQPAKOFPLISPPSSPSVGWKPISDATPVINYDLIYAVAKLGPGKELYHAGTESTPS 205
Qy	136 LLPPQPVKFLISPPSPASPVGKQSEDAMPVINYDLCAVSKLGPGKELYHAGTESTPS 195	Db 136 LLPPQPVKFLISPPSPASPVGKQSEDAMPVINYDLCAVSKLGPGKELYHAGTESTPS 195
Db	206 VVTHVCDSMERBEDPKTSPPKPKINOTRRPGLP 238	Qy 206 VVTHVCDSMERBEDPKTSPPKPKINOTRRPGLP 238
Qy	196 VVTHVCSETEEEETK-NPKQKTAQTRRDPP 227	Db 196 VVTHVCSETEEEETK-NPKQKTAQTRRDPP 227
Db	RESULT 1.2 AAE18918 ID AAE18918 Standard; protein; 212 AA.	RESULT 1.1 ADE37342 ID ADE37342 standard; protein; 241 AA.
XX	XX	XX
XX	AC AAE18918;	AC AAE18918;
XX	DT 17-MAY-2002 (first entry)	DT 17-MAY-2002 (first entry)

QY	55 LPNSLFACTVHQSYPEEEESKEKEPLFRTYDECUTFQLFKSPFRVRINFSPKSAARAR 114	Query	47.5%; Score 616; DB 5; Length 197;
Db	64 LPSATTACHLDPRFEVDGLCRAKESLPLPTYDKDITFQFKSPFRVRINFSPKSAARAR 123	Best Local Matches	No. 9. 8e-57; Mismatches 39; Indels 8; Gaps 2;
QY	115 IELHETOPFGKKLPLFYAQVQTPTEDGDKLHLAPPQAKQFLISPPSSPVGWKPISDAT 174	QY	51 DFSDFLPLNSLFACTVHQSYPEEEESKEKEPLFRTYDECUTFQLFKSPFRVRINFSPKSA 110
Db	124 LQHKHTEFGLKEMKLKYFAQTLHIGSS---HLAPPNPDKQFLISPPASPPVGWQV 179	Db	5 DLQDPLSATIACHLDPRFEVDGLCRAKESLPLPTYDKDITFQFKSPFRVRINFSPKSA 64
QY	175 PVINYDLVAVAKLGPGKELYELLAGTESTPSVVVHVCDSDMEREEDPKTS---PKPKIN 230	QY	111 ARARIELHETOFQKKLPLFYAQVQTPTDGDKLHLAPPQAKQFLISPPSSPVGWKP1 170
Db	180 PVINYDLVAVAKLGPGKELYELLAGTESTPSVVVHVCDSDMEREEDPKTS---PKPKIN 239	Db	65 ADARLQHKTKEFTGKEMKLKYFAQTLHIGSS---HLAPPNPDKQFLISPPASPPVGWQV 120
QY	231 QTRREGGLPP 239	QY	171 SDATPVINYDLVAVAKLGPGKELYELLAGTESTPSVVVHVCDSDMEREEDPKTS---PK 226
Db	240 QTRREBTP 248	Db	121 EDATPVINYDLVAVAKLGPGKELYELLAGTESTPSVVVHVCDSDMEREEDPKTS---PK 226
		QY	227 PKINOTRREGGLPP 239
		Db	181 PKIOTRREBTP 193
<hr/>			
RESULT 14			
AAC18915	AAE18915 standard; protein; 197 AA.	AAE18914	AAE18914 standard; protein; 197 AA.
XX		XX	
AC		AC	
XX		XX	
DT	17 MAY 2002 (first entry)	DT	17-MAY-2002 (first entry)
ID		ID	
DE	Human MCIP associated protein #2.	DE	Human MCIP associated protein #1.
XX		XX	
KW	Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy; heart failure; cardiomyopathy; heart disease; human.	KW	Muscle calcineurin interacting protein; MCIP; cardiac hypertrophy; heart failure; cardiomyopathy; heart disease; human.
XX		XX	
OS	Homo Sapiens.	OS	Homo sapiens.
PN	WO200204491-A2.	PN	WO200204491-A2.
XX		XX	
PD	17-JAN-2002.	PD	17-JAN-2002.
XX		XX	
PF	06-JUL-2001; 2001WO-US0216652.	PF	06-JUL-2001; 2001WO-US0216652.
XX		XX	
PR	07-JUL-2000; 2000US-0216601P.	PR	07-JUL-2000; 2000US-0216601P.
XX		XX	
PR	13-FEB-2001; 2001US-00782953.	PR	13-FEB-2001; 2001US-00782953.
XX		XX	
PA	(TEXA) UNIV TEXAS SYSTEM.	PA	(TEXA) UNIV TEXAS SYSTEM.
PA	(WILL/) WILLIAMS S R.	PA	(WILL/) WILLIAMS S R.
PA	(ROTH/) ROTHERMEL B.	PA	(ROTH/) ROTHERMEL B.
XX		XX	
PI	Williams SR, Rothermel B;	PI	Williams SR, Rothermel B;
XX		XX	
DR	WPI; 2002-179698/23.	DR	WPI; 2002-179698/23.
N-PSDB	AAD30156.	N-PSDB	AAD30155.
XX		XX	
PT	Screening for modulators of muscle calcineurin interacting protein (MCIP) binding, expression or phosphorylation, useful for treating cardiac hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a test compound.	PT	Screening for modulators of muscle calcineurin interacting protein (MCIP) binding, expression or phosphorylation, useful for treating cardiac hypertrophy or heart failure, comprises mixing MCIP, calcineurin and a test compound.
XX		XX	
PS	Example 1; Page 161-162; 174pp; English.	PS	Example 1; Page 157-158; 174pp; English.
XX		XX	
CC	The invention relates to muscle calcineurin interacting proteins (MCIPs) and nucleic acid molecules encoding such proteins. MCIPs form a physical complex with the catalytic subunit of calcineurin and increased levels of MCIPs correspond to a reduced ability of calcineurin to stimulate transcription of certain target genes. The invention also relates to methods for identifying modulators of MCIP binding, expression or phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin may be used for treating cardiac hypertrophy and heart failure.	CC	The invention relates to muscle calcineurin interacting proteins (MCIPs) and nucleic acid molecules encoding such proteins. MCIPs form a physical complex with the catalytic subunit of calcineurin and increased levels of MCIPs correspond to a reduced ability of calcineurin to stimulate transcription of certain target genes. The invention also relates to methods for identifying modulators of MCIP binding, expression or phosphorylation. Inhibitors or promoters of MCIP binding to calcineurin may be used for treating cardiac hypertrophy and heart failure.
CC	Antibodies to MCIP can be used in characterising the MCIP content of healthy and diseased tissues and subsequently for determining the presence or absence of cardiomyopathy as predictor of heart disease. The present sequence is human MCIP associated protein. Note: This sequence has been described as murine MCIP splice variant in the specification, however the sequence seems to be a MCIP associated protein sequence 197 AA;	CC	Antibodies to MCIP can be used in characterising the MCIP content of healthy and diseased tissues and subsequently for determining the presence or absence of cardiomyopathy or as predictor of heart disease.
SQ		SQ	

The present sequence is human MCIP associated protein. Note: This sequence has been described as murine splice variant in the specification, however the sequence seems to be a MCIP associated protein isoform. Sequence 197 AA:

Qy	Query	Match	47.5%	Score 616;	DB 5;	Length 197;
	Best Local Similarity	62.6%		Pred. No. 9	8e-57;	
	Matches 117;	Conservative	27;	Mismatches	35;	Indels 8;
				Gaps	2	
Qy	57	NSIFACNYHOSYPEEEESKEKPFEGLFRTYDECYTOLFKSFRVRVINFSHPKSAAPARIE 116	:			
Ddb	11	SSLACVANSDISSSETRAKFSLFRYDQDITQFKEKSFRVRVINFNSNPSAADRLQ 70	SSLACVANSDISSSETRAKFSLFRYDQDITQFKEKSFRVRVINFNSNPSAADRLQ			
Qy	117	LHETOFGRKKLPLFYAQVQTPEIDGDKLHLAPPQAKQFLISPPSSPSVGWKPISDAPV 176	LHETOFGRKKLPLFYAQVQTPEIDGDKLHLAPPQAKQFLISPPSSPSVGWKPISDAPV			
Ddb	71	LHKCFEGLMCKLYFAQLTHIGSS --- -HLAPNPNDQFLISPPASPVGPWKQVOEDAPV 126	LHKCFEGLMCKLYFAQLTHIGSS --- -HLAPNPNDQFLISPPASPVGPWKQVOEDAPV			
Qy	177	INVDLLYAVAKLGPGKEXYELHAAGTESTPSVWVHVCDSDMERBEDPPTS --- -PKPKINOT 232	INVDLLYAVAKLGPGKEXYELHAAGTESTPSVWVHVCDSDMERBEDPPTS --- -PKPKINOT			
Ddb	127	INVDLLYAIKSLGPGKEXYELHAATDTTPSVWVHVCESDQEKEEEEMERMRPKPKIOT 186	INVDLLYAIKSLGPGKEXYELHAATDTTPSVWVHVCESDQEKEEEEMERMRPKPKIOT			
Qy	233	RRCPLPP 239	RRCPLPP			
Ddb	187	RRPBYP 193	RRPBYP			

Search completed: November 16, 2005, 16:47:32
Job time : 126.95 secs

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Om protein - protein search, using sw model

Run on: November 16, 2005, 16:22:55 ; Search time 33 Seconds

(without alignments)
547.426 Million cell updates/sec

Title: US-09-575-580B-5

Perfect score: 1296

Sequence: 1 EFVDPVRPRVRLQQASIP.....TSPPKPKINQTRRPGLPPFGH 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Maximum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

Database : Issued Patents AA:
 1: /cgpn2_6/prodata/1/iaa/5A.COMB.pep:
 2: /cgpn2_6/prodata/1/iaa/5B.COMB.pep:
 3: /cgpn2_6/prodata/1/iaa/6A.COMB.pep:
 4: /cgpn2_6/prodata/1/iaa/6B.COMB.pep:
 5: /cgpn2_6/prodata/1/iaa/PCUTUS.COMB.pep:
 6: /cgpn2_6/prodata/1/iaa/backfiles.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1129	87.1	255	4	US-09-614-474-2
2	861	65.4	206	4	US-09-949-016-11450
3	848	65.4	192	4	US-09-614-474-10
4	848	63.4	192	4	US-09-949-016-6559
5	708.5	54.7	241	4	US-09-614-474-11
6	708.5	54.7	248	4	US-09-949-016-7081
7	575	44.4	171	4	US-09-949-016-6493
8	575	44.4	173	4	US-09-949-016-11053
9	565	43.6	171	2	US-08-665-040-2
10	405.5	31.3	289	4	US-09-27-076-44503
11	312	24.1	111	4	US-09-513-399C-5849
12	106.5	8.2	285	4	US-09-248-996A-19049
13	106.5	8.2	767	4	US-09-252-991A-15612
14	94	7.3	655	3	US-09-347-333-4
15	89	6.9	905	2	US-08-574-059A-9
16	89	6.9	905	3	US-09-357-014-9
17	89	6.9	1135	2	US-08-574-059A-7
18	89	6.9	1135	3	US-09-357-014-7
19	88.5	6.8	782	4	US-09-252-991A-30464
20	88.5	6.8	4019	4	US-09-854-133-435
21	85	6.6	454	3	US-08-348-118C-4
22	85	6.6	454	3	US-08-476-509B-4
23	84.5	6.5	1106	1	US-08-180-195-2
24	84.5	6.5	1106	1	US-08-168-317-2
25	84.5	6.5	1106	1	US-08-477-329-2
26	84.5	6.5	1106	2	US-08-475-58-2
27	84.5	6.5	1106	2	US-08-460-510-2

Total number of hits satisfying chosen parameters:

513545

ALIGNMENTS

RESULT 1
US-09-614-474-2
; Sequence 2, Application US/09614474
; Patent No. 6524919
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tirgley, Debora W.
; APPLICANT: Edwards, Carla M.
; APPLICANT: Streeter, David G.
; TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION 1-LIKE PROTEINS
; FILE REFERENCE: PC-0013 US
; CURRENT APPLICATION NUMBER: US/09/614,474
; CURRENT FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PERL Program
SEQ ID NO: 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyc ID No. 6524819 247500.5
; NAME/KEY: unsure
; LOCATION: 11
; OTHER INFORMATION: unknown or other
US-09-614-474-2

Query Match 87.1%; Score 1129; DB 4; Length 255;
Best Local Similarity 92.5%; Pred. No. 1 5e-121;
Matches 209; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
Query Match 87.1%; Score 1129; DB 4; Length 255;
Best Local Similarity 92.5%; Pred. No. 1 5e-121;
Matches 209; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
QY 14 GQOASIPENGGLPFLCCIDRDWATQCFABEEAFQALTDSDLPLNSLFACNVHQSVFEEB 73
Db 26 GQOHPVEPDGLPFLCCIDRDWATRCPFAEFAITDNDLPLSLFAGNVHQVFEGEB 85
QY 14 GQOASIPENGGLPFLCCIDRDWATQCFABEEAFQALTDSDLPLNSLFACNVHQSVFEEB 73
Db 26 GQOHPVEPDGLPFLCCIDRDWATRCPFAEFAITDNDLPLSLFAGNVHQVFEGEB 85
QY 74 SKERFEGLFRTYDCVTFQFKSPPRVINFSHKSAAARARIEHHETQFRGKLLPLYFAQ 133
Db 86 SKERFEGLFRTYDCVTFQFKSPPRVINFNSNKSAAARARIEHHETQFRGKLLLYFAQ 145
QY 134 VQTPTDGDKLHLAPPQPAQFLISPPSSPSVGKWPISDAPVUNYDLYAVAKLGPEK 193
Db 146 VQTPTDGDKLHLAPPQPAQFLISPPSSPSVGKWPISDAPVUNYDLYAVAKLGPEK 205
QY 194 YEHLAGTESTPSVWVHCDMREBEDPDTSPSKPKINOTRPGLPP 239
Db 206 YEHLAGTESTPSVWVHCDMREBEDPDTSPSKPKIIQRRPGLPP 251
RESULT 2
US-09-949-016-11450

Sequence 11450, Application US/09949016
 Patent No. 6812339

GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 11450
 LENGTH: 206
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-11450

Query Match 66.4%; Score 861; DB 4; Length 206;
 Best Local Similarity 89.1%; Prod. No. 8.3e-9;
 Matches 163; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 57 NSLFACNTHQSVPFEEEEEKEKFGFLFRTYDECVTQFLFKSFRVRINSHPKSAARARIE 116
 Db 20 STLVACVVDVEFTNQEVKEKFGFLFRYDDCVTFQFLFKSFRVRINSHPKSAARARIE 79

Qy 117 LHETQFRGKLPFLYFAQVOTPEFDGDKLHLAPPQAKQFLISPPSSPSVGKWPISDATPV 176
 Db 80 LHETQFRGKLPFLYFAQVOTPEFDGDKLHLAPPQAKQFLISPPSSPSVGKWPISDATPV 139

Qy 177 LNYDLYAVAKLGPGKELYELHAGTESTPSVYHVCDSDMEREEDPKTSPKKINQPRPG 236
 Db 140 LNYDLYAVAKLGPGKELYELHAGTESTPSVYHVCDSDIEEBDPKTSPKKIIQTRPG 199

Qy 237 LPP 239
 Db 200 LPP 202

RESULT 3
 US-09-614-474-10
 Sequence 1.0, Application US/09614474
 Patent No. 6524819

GENERAL INFORMATION:
 APPLICANT: Loring, Jeanne F.
 APPLICANT: Tingley, Debora W.
 APPLICANT: Edwards, Carla M.
 APPLICANT: Streeter, David G.
 TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION 1-LIKE PROTEINS
 FILE REFERENCE: PC-0013 US
 CURRENT APPLICATION NUMBER: US/09/614,474
 CURRENT FILING DATE: 2000-07-11
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: PERL Program
 LENGTH: 192
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: misc feature
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No. 6524819 g1435040

Query Match 65.4%; Score 848; DB 4; Length 192;
 Best Local Similarity 88.0%; Prod. No. 2.3e-8;
 Matches 161; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

US-09-614-474-10
 57 NSLFACNTHQSVPFEEEEEKEKFGFLFRTYDECVTQFLFKSFRVRINSHPKSAARARIE 116

Db CURRENT APPLICATION NUMBER: US/09/614,474
; CURRENT FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PERL program
SEQ ID NO: 11
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6524819 96017919
US-09-614-474-11

Query Match 54.7%; Score 708.5; DB 4; Length 241;
Best Local Similarity 66.2%; Fred. No. 3.9e-73;
Matches 141; Conservative 20; Mismatches 49; Indels 3; Gaps 2;

Qy 28 LCCIDBDWAVTQCFA -EEAFOALTDPSDLNLSFACNYHQSVPEEESEKEFGLFRTY 85
| :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
| 16 LCSTDQEEEEMIFGENEDDIDMDSLDLTSFACSVHAEVFAAREQERFEALFTY 75
Db 86 DECUTPQLFKSFRRVINFSHPKSAAARARLELHETOFRGKLLPLYFAQVOTPETDGDKLH 145
| :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
| 76 DDQVTFQLFKSFRRVINFSHPKSPEEARPARLELHEDFNGKLKLYFAQVOMSGEVRDKEY 135
Db 146 LAPPQAKOFLLSPPSPSYCWKPISDATPVLNYDLYAYAKLGPGEKYELHAGTESTPS 205
| :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
| 136 LLPPQVKQFLLSPSPVWQKQSADMPVINYDLCAVSKLGGEKYELHAGTESTPS 195
Db 206 VVHVCESETTEBEEBETK-NPQKIAQTRRPPPP 238
| :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 196 VVHVCESETTEBEEBETK-NPQKIAQTRRPPPP 227
| :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
; SEQ ID NO: 7081 Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 7081
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7081

RESULT 6
US-09-949-016-7081 Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 7081
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7081

Query Match 54.7%; Score 708.5; DB 4; Length 248;
Best Local Similarity 66.2%; Fred. No. 4e-73;
Matches 141; Conservative 20; Mismatches 49; Indels 3; Gaps 2;

Qy 28 LCCIDBDWAVTQCFA -EEAFOALTDPSDLNLSFACNYHQSVPEEESEKEFGLFRTY 85
| :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
| 23 LCSTDQEEEEMIFGENEDDIDMDSLDLTSFACSVHAEVFAAREQERFEALFTY 82
Db 86 DECUTPQLFKSFRRVINFSHPKSAAARARLELHETOFRGKLLPLYFAQVOTPETDGDKLH 145
| :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
| 83 DDQVTFQLFKSFRRVINFSHPKSPEEARPARLELHEDFNGKLKLYFAQVOMSGEVRDKEY 142
Db 146 LAPPQAKOFLLSPPSPSYCWKPISDATPVLNYDLYAYAKLGPGEKYELHAGTESTPS 205
| :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
; SEQ ID NO: 7081 Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 11053
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11053

RESULT 7
US-09-949-016-6493
; Sequence 6453, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 60/231,498
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 6493
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6493

Query Match 44.4%; Score 575; DB 4; Length 171;
Best Local Similarity 65.9%; Pred. No. 5.5e-58;
Matches 110; Conservative 22; Mismatches 27; Indels 8; Gaps 2;

Qy 77 KFEGFLFRTYDECUTPQLFKSFRRVINFSHPKSAAARARLELHETOFRGKLLPLYFAQVOT 136
| :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 5 KFESLFRTYDKDITQFVKSFRRVINFSNPFSIADARIQLHKTBFLGEMKLYFAQTLH 64
; SEQ ID NO: 6493
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6493

Query Match 44.4%; Score 575; DB 4; Length 171;
Best Local Similarity 65.9%; Pred. No. 5.5e-58;
Matches 110; Conservative 22; Mismatches 27; Indels 8; Gaps 2;

Qy 137 PETGDKLHLAPPQAKOFLLSPPSPSYCWKPISDATPVLNYDLYAYAKLGPGEKYEL 196
| :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 65 IGSS---HLAPPNPDKQPLISPPASPPVGKQVBDATEVINYDLYAYAKLGPGEKYEL 120
; SEQ ID NO: 6493
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6493

Query Match 44.4%; Score 575; DB 4; Length 171;
Best Local Similarity 65.9%; Pred. No. 5.5e-58;
Matches 110; Conservative 22; Mismatches 27; Indels 8; Gaps 2;

Qy 197 HAGTESTPSVYVHYCDSMREREPPKTS --- PKPKTKNOTRRPPLPP 239
| :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 121 HAATDTTPSVVHYCSESDQEKEEBEMMRPKPKIOTRRPEYTP 167
; SEQ ID NO: 6493
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6493

RESULT 8
US-09-949-016-11053
; Sequence 11053, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 11053
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11053

Query Match 54.7%; Score 708.5; DB 4; Length 248;
Best Local Similarity 66.2%; Fred. No. 4e-73;
Matches 141; Conservative 20; Mismatches 49; Indels 3; Gaps 2;

Qy 28 LCCIDBDWAVTQCFA -EEAFOALTDPSDLNLSFACNYHQSVPEEESEKEFGLFRTY 85
| :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
| 23 LCSTDQEEEEMIFGENEDDIDMDSLDLTSFACSVHAEVFAAREQERFEALFTY 82
Db 86 DECUTPQLFKSFRRVINFSHPKSAAARARLELHETOFRGKLLPLYFAQVOTPETDGDKLH 145
| :|||:|||:|||:|||:|||:|||:|||:|||:|||:
| 83 DDQVTFQLFKSFRRVINFSHPKSPEEARPARLELHEDFNGKLKLYFAQVOMSGEVRDKEY 142
Db 146 LAPPQAKOFLLSPPSPSYCWKPISDATPVLNYDLYAYAKLGPGEKYELHAGTESTPS 205
| :|||:|||:|||:|||:|||:|||:|||:
; SEQ ID NO: 7081 Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 11053
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11053

Query Match 44.4%; Score 575; DB 4; Length 173;
 Best Local Similarity 65.9%; Pred. No. 5.6e-58
 Matches 110; Conservative 22; Mismatches 27; Indels 8; Gaps 2;

Qy ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 77 KFEGLFRYDECVTQFLPKSFRVRINFSHPKSAARARIELHETOFRGKKLPLFYAQVQT 136

Db ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
 7 KFESLFRYDKDITFQYFKSFRVRINFSNPFSAAARLQLIHKTEFGKEMKLHYFACTLH 66

Qy 137 PETDGDKLHLAPPQAKQFLISPPSSPSVGKPKISDATPVINYDLIYAVAKLGPGKELY 196

Db 67 1GSS---HLAPPNPKQFLISPPSSPSVGKPKISDATPVINYDLIYAVAKLGPGKELY 196

Qy 197 HAGTESTPSVWVHVCSQKEEEEMMRMRSKPKTQTRPEYTP 167

Db 123 HAATDTPSVWVHVCSQKEEEEMMRMRSKPKTQTRPEYTP 169

RESULT 10
 US-09-270-767-44503
 Sequence 44503, Application US/09270767
 Patent No. 6703491
 GENERAL INFORMATION:
 / APPLICANT: Homburger et al.
 / TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 / FILE REFERENCE: 7326-094
 / CURRENT APPLICATION NUMBER: US/09/270,767
 / CURRENT FILING DATE: 1999-03-17
 / NUMBER OF SEQ ID NOS: 62517
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO: 44503
 / LENGTH: 289
 / TYPE: PRT
 / ORGANISM: *Drosophila melanogaster*

Query Match 31.3%; Score 405.5; DB 4;
 Best Local Similarity 41.2%; Pred. No. 4.1e-38;
 Matches 89; Conservative 32; Mismatches 74; Indels 21; Gaps 6;

Qy 15 QOASIPEDGGLFFLCCIDRDWAVTQFAAEFAQLTDSDLPNSLACNYHQSVFREES 74
 Db 94 QHPSLPEQED-----VPSD-----TEPEVDA-DSFDDLPSTSIVTNLHSVPANEL 139

Qy 75 RERFEGIFRTYDECVTQFLPKSFRVRINFSHPKSAARARIELHETOFRGKK-LPIYFAQ 133
 Db 140 KHAMEELFRTSSEAFQMLRSFRRLRVNTDNAIAANANARIKLHQYEENKKTIVTCYFAQ 199

Qy 134 VQTPTEDGDKLHLAPPQAKQFLISPPSSPSVGKPKISDATPVINYDLIYAVAKLGPGK 193
 Db 200 PVTPVSN---KNLQPPAPVTKLSPASPPAGWPREEGEPLVNHDLLAALASLTPGES 256

Qy 194 YBLHAGTESTPSVWVHVCSQKEEEEMMRMRSKPKTQTRPEYTP 229

Db 257 HELPOSEDQPAIVHTA--MLAETGPGLQYKAPI 289

RESULT 11
 US-09-513-999C-5849
 Sequence 5849, Application US/09513999C
 Patent No. 6783961
 GENERAL INFORMATION:
 / APPLICANT: Dumas Milne Edwards, J.B.
 / ATTORNEY/AGENT INFORMATION:
 NAME: JANET L. CORD
 REGISTRATION NUMBER: 33,778
 REFERENCE DOCKET NUMBER: U010815-9
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 708-1810
 TELEFAX: (212) 246-8959
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 171 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide

US-09-665-040-2

Query Match 43.6%; Score 565; DB 2; Length 171;
 Best Local Similarity 65.3%; Pred. No. 7.8e-57;
 Matches 109; Conservative 22; Mismatches 28; Indels 8; Gaps 2;

Qy 77 KFEGLFRYDECVTQFLPKSFRVRINFSHPKSAARARIELHETOFRGKKLPLFYAQVQT 136

Query Match 24.1%; Score 312; DB 4; Length 111;
 Best Local Similarity 58.1%; Prod. No. 5; 6e-28;
 Matches 61; Conservative 17; Mismatches 22; Indels 4; Gaps 1;

Qy 57 NSLPACNYHOSVFRBEESKEKPFEGLFRYDECYTFOLFKSFRVRINPSHPKSAARARIE 116
 Db 11 SSSLTACVANSDFSESETRAKFESLFRYDKDITFQYXPKSFRVRINSNPFSAA达尔Q 70

Query 117 LHETOPIRGKPLKLYFAQVQTPTEDGDKMLAPPAPAKFLISPPS 161
 Db 71 LHKTEFLGKEMKLKYFACTLHIGSS---HLAPPNPDKQFLISPPA 111

RESULT 12
 US-09-248-796A-19049
 ; Sequence 19049, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Wainstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 ; FILE REFERENCE: 101196-132
 ; CURRENT APPLICATION NUMBER: US/09/248,796A
 ; PRIORITY FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 19049
 ; LENGTH: 285
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 ; FEATURE:
 ; NAME/KEY: UNSURE
 ; LOCATION: (282)
 ; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown

Query Match 8.2%; Score 106.5; DB 4; Length 767;
 Best Local Similarity 23.2%; Prod. No. 0.005; Mismatches 35; Indels 39; Gaps 8;
 Matches 45; Conservative 35; Mismatches 75; Indels 39; Gaps 8;

Qy 63 NYHQSVFREESKEK--PEGLFLR-TYD-----ECYTFOLFKS-FRRVRINFSH 106
 Db 240 DMETVFDQKKPKQSNFEKKLKRKHNDVHPPIERTIQKOBQDIDWATPKSDINRMNLSLTSH 299

Query 107 PKSAARARIELHETQFRGKPLFYAQVQTPTEDG--DKLHLAPPAPAKQFLISPPSSP 163
 Db 300 DKSRTRXVRVRODGSIIVKPLD-FISEINTNTVGPDDDDILENVQYSK-----348

Query 164 SVGMKPISDATPVNLNYDLYAYAKLGPEKYLHAGT-ESTPSVYVHCDSDMEREEDPK 222
 Db 349 -----IETFWLNYDLSYDNLISIKFHSSVINOVRCLVHLCKFDIETTSKI 400

Query 223 TSPKPKINOTRRPG 236
 Db 401 LQQKPKLSEAQHSG 414

RESULT 14
 US-09-347-833-4
 ; Sequence 4, Application US/09347833
 ; Patent No. 6294658

GENERAL INFORMATION:
 ; APPLICANT: Fanodou, Layo O.
 ; INVENTION: Factors Involved in Gene Expression
 ; FILE REFERENCE: BB-1172
 ; CURRENT APPLICATION NUMBER: US/09/347,833
 ; CURRENT FILING DATE: 1999-07-02
 ; EARLIER APPLICATION NUMBER: 60/032,415
 ; EARLIER FILING DATE: July 10, 1998
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 4
 ; LENGTH: 655
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown

Query Match 7.3%; Score 94; DB 3; Length 655;
 Best Local Similarity 21.4%; Prod. No. 0.11; Mismatches 91; Indels 78; Gaps 13;
 Matches 55; Conservative 33; Mismatches 91; Indels 78; Gaps 13;

Qy 32 DRDWAVTQCFAE-----EAFOA-LTDPSD--LPNSLFACTVNHQSVPBEESEBKFP 78
 Db 280 DREWYV-CRAQRKSKERBMLKBFERNIKEADRNQGNTNLTKNLDSIDDEKLKEIF 337

Query 79 EQLFRTYDECYTFOLFKSFRVR-----INFSHPKSAARARIELHETQFRGKPLPLYFAQ 133
 Db 338 AD-FGTITSC---KVMRDNGYSKGSGFVAPKSAEDASRALYANGRMIGSK--PLVAL 391

Query 134 VOPTETODKLH-----LAPQIAKQFLISPPSPSVWKPISDATPVLYDILYA 184
 Db 392 AQRKEERRARLQAQFSQMRPMPPVPSAPRMMPYPPGVPGVQGQPPP-----A 444

Query 185 VAKLGPEKYLHAGTTESTPSVYVHCDSDMEREEDPKTSP----KPKINOTRRPGLP-
 ; Sequence 15612, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Wainstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 ; FILE REFERENCE: 101196-132
 ; CURRENT APPLICATION NUMBER: US/09/248,796A
 ; NUMBER OF SEQ ID NOS: 28208
 ; PRIORITY APPLICATION NUMBER: US 60/074,725
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/096,409

RESULT 15
US-08-574-959A-9

Sequence 9, Application US/08574959A
Patent No. 596224

GENERAL INFORMATION:

APPLICANT: Jaekyoon Shin, Inseil Joung, Ratna K. Vadlamudi
TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: LARIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/574,959A
FILING DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 905 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-574-959A-9

Query Match 6.9%; Score 89; DB 2; Length 905;
Best Local Similarity 24.0%; Pred. No. 0.66; Length 905;
Matches 41; Conservative 16; Mismatches 82; Indels 32; Gaps 5;

Qy 70 EEEESKEKFEGLFRTYDECVTQFLFKSFRRYRINFSHPKSAAARARIELHETQFRGKPL 129
Db 698 EEEEEEEEEEFFFFEEEEE^G
Qy 130 YFAQVQTPETDGDKLHAPPQAKQFLISPPSSPSVGMKPSIDATPVLYNYLILYAYAKLG 189
Db 737 --DLEFRTAGGVEE^GAPPPTLPPALPPBSP--PKVQPEBSPBPGILLEVE-- 786
Qy 190 PGEKYELHAGCTESTPSVYHVCDSDMRE-EDPKTSBPKINOTRRPGLPP 239
Db 787 PETEEERGADTAPTLAPEALPSQEGEREGBPAAGPPQELVEEFSSXPP 837

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RESULT 2
 US-10-290-438-2
 Sequence 2, Application US/10290438
 Publication No. US20030186333A1
 GENERAL INFORMATION
 APPLICANT: Lorring, Jeanne F.
 APPLICANT: Tingley, Debra W.
 APPLICANT: Edward, Carla M.
 APPLICANT: Streeter, David G.
 TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION 1-LIKE PROTEIN
 FILE REFERENCE: PC-0013-1CIP
 CURRENT APPLICATION NUMBER: US/10/290,438
 CURRENT FILING DATE: 2002-11-06
 PRIOR APPLICATION NUMBER: 07/614,474
 PRIOR FILING DATE: 2000-07-11
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: PERL Program
 SEQ ID NO: 2
 LENGTH: 255
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: misc feature
 NAME/KEY: OTHER INFORMATION: Incyte ID No. US20030186333A1 247500-5
 FEATURE:
 NAME/KEY: unsure
 LOCATION: 11
 OTHER INFORMATION: unknown or other
 US-10-290-438-2

Query Match 87.1%; Score 1129; DB 14; Length 255;
 Best Local Similarity 92.5%; Pred. No. 2_3e-105;
 Matches 209; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 14 GQQASIDPEGGFLPLCCIDRQWATQCFAEEAFAQALTDPSLNSLFACNHQSYFEE 73
 Db 26 GQGHHVFDGGFLPLCCIDRQWATRCFAEEAFAQALTDENDLPSLFACNHQSYFEGEE 85

Qy 74 SKEKFEGIERTYDECVTOLFQSFRVRINFSPKSAARARTELHTQFRSKLPLYFAQ 133
 Db 86 SKEKFEGIERTYDDCVTFQFLQSFRVRINFSPNPKSAARARTELHTQFRSKKLKYPAQ 145

Qy 134 VOTPETDQDKLHLAPPQAKOFLISPPSSPGWKPISDATPVLYNDLLYAVAKLGPGEK 193
 Db 146 VOTPETDQDKLHLAPPQAKOFLISPPSSPGWQPINDATPVLYNDLLYAVAKLGPBK 205

Qy 194 YELHAGTTESTPSVYHYCDSDMEREEDPQTSPKPKINQTRRGLPP 239
 Db 206 YELHAGTTESTPSVYHYCDSDIEEEEDPQTSPKPKIQTQTRRGLPP 251

RESULT 3
 US-09-782-953-9
 Sequence 9, Application US/09782953
 GENERAL INFORMATION
 APPLICANT: WILLIAMS, R. SANDERS
 APPLICANT: ROTHERMEL, BEVERLY
 TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
 FILE REFERENCE: US/09/782,953
 CURRENT APPLICATION NUMBER: US/09/782,953
 CURRENT FILING DATE: 2001-02-13
 PRIOR APPLICATION NUMBER: 60/216,601
 PRIOR FILING DATE: 2000-07-07
 NUMBER OF SEQ ID NOS: 27
 SEQ ID NO: 10
 LENGTH: 197
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-782-953-10

Query Match 68.1%; Score 882; DB 9; Length 197;
 Best Local Similarity 91.8%; Pred. No. 1.5e-80;
 Matches 168; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

Qy 57 NSLFACNVHQSYFEEBESKEKPEGIERTYDECVTOLFQSFRVRINFSPKSAARARIE 116
 Db 11 STLVACTVDEVFNTQEVKPEGIERTYDECVTOLFQSFRVRINFSPKSAARARIE 70

Qy 117 LHETQFRGKQLPLYFAQVQTPETDQDKLHLAPPQAKOFLISPPSSPGWKPISDATPV 176
 Db 71 LHETQFRGKQLKLYFAQVQTPETDQDKLHLAPPQAKOFLISPPSSPGWKPISDATPV 130

Qy 177 LNYDLYYAVAKLGPGEKYLHAGTESTPSVYHYCDSDMEREEDPQTSPKPKINGQTRRPG 236
 Db 131 LNYDLYYAVAKLGPGEKYLHAGTESTPSVYHYCDSDMEEEDPQTSPKPKIQTQTRRPG 190

Qy 237 LPP 239
 Db 191 LPP 193

RESULT 5
 US-09-782-953-18

Sequence 18, Application US/09782953
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; TITLE OF INVENTION: CALCINEURIN INTERACTING PROTEIN (MCIP)
; FILE REFERENCE: UTSID:674PZ1
; CURRENT APPLICATION NUMBER: US/09/782,953
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/216,601
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE ID NO: 18
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-782-953-18

Query Match 65.4%; Score 848; DB 9; Length 192;
Best Local Similarity 88.0%; Pred. No. 3.9e-77;
Matches 161; Conservative 8; Indels 0; Gaps 0;

Qy 57 NSLPACNTHQSVPFEEESKEKEFGLFRTYDECYTFOLFKSFRVRINFSHPKSAARARIE 116
Db 6 STLVACVVDVEPTNQETKEKEFGLFRTYDDCYTFOLFKSFRVRINFSNPNSPKSAARARIE 65

Qy 117 LHETQFRGKLLPFLYPAQVQTPETDGKLHAPQPAOKFLISPPSSPGWKPISDATPV 176
Db 66 LHETQFRGKLLPFLYPAQVQTPETDGKLHAPQPAOKFLISPPSSPGWKPISDATPV 125

Qy 177 LNDDLLYAVAKLGKGEKEYLHAGTESTPSVWVHCDSDMEREDPKTSPKPKINOTRPG 236
Db 126 LNDDLLYAVAKLGKGEKEYLHAGTESTPSVWVHCDSDIEEEEDEPKTSPKPKLIQTRPG 185

Qy 237 LPP 239
Db 186 LPP 188

RESULT 7
US-10-290-438-10
; Sequence 10, Application US/10290438
; Publication No. US2003018633A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debra W.
; APPLICANT: Edwards, Carla M.
; APPLICANT: Streeter, David G.
; TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION 1-LIKE PROTEIN
; FILE REFERENCE: PC-0013-1CIP
; CURRENT APPLICATION NUMBER: US/10/290,438
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 09/614,474
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PERL Program
; SEQ ID NO: 10
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: m8c feature
; OTHER INFORMATION: Incyte ID No. US2003018633A1 91435040
US-10-290-438-10

Query Match 65.4%; Score 848; DB 14; Length 192;
Best Local Similarity 88.0%; Pred. No. 3.9e-77;
Matches 161; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

Qy 57 NSLPACNTHQSVPFEEESKEKEFGLFRTYDECYTFOLFKSFRVRINFSHPKSAARARIE 116
Db 6 STLVACVVDVEPTNQEVKEFGLFRYDDCYTFOLFKSFRVRINFSNPNSPKSAARARIE 65

Qy 117 LHETQFRGKLLPFLYPAQVQTPETDGKLHAPQPAOKFLISPPSSPGWKPISDATPV 176
Db 66 LHETQFRGKLLPFLYPAQVQTPETDGKLHAPQPAOKFLISPPSSPGWKPISDATPV 125

Qy 177 LNDDLLYAVAKLGKGEKEYLHAGTESTPSVWVHCDSDMEREDPKTSPKPKINOTRPG 236
Db 126 LNDDLLYAVAKLGKGEKEYLHAGTESTPSVWVHCDSDIEEEEDEPKTSPKPKLIQTRPG 185

Qy 237 LPP 239
Db 186 LPP 188

RESULT 8
US-10-764-425-126
; Sequence 126, Application US/10764425
; Publication No. US2004014692A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Eveleigh, Deepa
; APPLICANT: Bigwood, Douglas
; APPLICANT: Taylor, Ian
; TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
; FILE REFERENCE: 5151
; CURRENT APPLICATION NUMBER: US/10/764,425
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/764,425
; PRIOR FILING DATE: 2003-01-24

Query Match 65.4%; Score 848; DB 9; Length 192;
Best Local Similarity 88.0%; Pred. No. 3.9e-77;
Matches 161; Conservative 8; Indels 0; Gaps 0;

Qy 57 NSLPACNTHQSVPFEEESKEKEFGLFRTYDECYTFOLFKSFRVRINFSHPKSAARARIE 116
Db 6 STLVACVVDVEPTNQEVKEFGLFRYDDCYTFOLFKSFRVRINFSNPNSPKSAARARIE 65

Qy 117 LHETQFRGKLLPFLYPAQVQTPETDGKLHAPQPAOKFLISPPSSPGWKPISDATPV 176

NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 126
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-45-126

Query Match 65.4% Score 848; DB 18; Length 197;
Best Local Similarity 88.0%; Pred. No. 4e-77; Indels 0; Gaps 0;
Matches 161; Conservative 8; Mismatches 14; Gaps 0;

Qy 57 NSLFA�HQSVEEESEKSFKEPGLFRTYDECYTFOLFKSFRVRINFSHPKSAARARIE 116
Db 11 STIVACVVDVEVTINQEYKEKGLFRTYDECYTFOLFKSFRVRINFSNPKSAARIE 70

Qy 117 LHETQPRGKCLPLFYAQVOTPETDGDKLHLAPPQAKQFLISPPSSPSVGWKPISDATPV 176
Db 71 LHETQFRERKLKLYFAQVOTPETDGDKLHLAPPQAKQFLISPPSSPSVGWKPISDATPV 130

Qy 177 LNFDLLAVAKLGPGKELYELHAGTESTSVVVHVCDSDMEREEDPKTSPKPKINQTRPG 236
Db 131 LNFDLLAVAKLGPGKELYELHAGTESTSVVVHVCDSDMEREEDPKTSPKPKIIQTRPG 190

Qy 237 LPP 239
Db 191 LPP 193

RESULT 9
US-09-782-953-21
; Sequence 11, Application US/09782953
; Patent No. US20020150953A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, R. SANDERS
; APPLICANT: ROTHERMEL, BEVERLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE
; TITLE OF INVENTION: CALCINEURIN INTERACTING PROTEIN (MCIP)
; FILE REFERENCE: USID: 674PZI
; CURRENT APPLICATION NUMBER: US/09/782, 953
; PRIORITY APPLICATION NUMBER: US/09/782, 953
; PRIORITY FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 21
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-953-21

Query Match 54.7% Score 708.5; DB 9; Length 241;
Best Local Similarity 66.2%; Pred. No. 6.e-63; Indels 3; Gaps 2;
Matches 141; Conservative 20; Mismatches 49; Gaps 2;

Qy 28 LCCIDRDAVTOCFA--EAFQALTDPSDLPNSLFA�CNVHSVPEEESEKSFEGLFRTY 85
Db 16 LSTDQEEEMIFGENDDDEMPSDLPNSLFA�CNVHSVPEEESEKSFEGLFRTY 75

Qy 86 DECYTFOLFKSFRVRINFSHPKSAARARIELHETQFRGKCLPLFYAQVOTPETDGDKLH 145
Db 76 DDQVTFOLFKSFRVRINFSKPEAAARARIELHETDNGQKLKLYPAQVOMSGEVRSKY 135

Qy 146 LAPPQAKQFLISPPSSPSVGWKPISDATPVLYAKLGPGKELYELHAGTESTPS 205
Db 136 LJPQPQPKQFLISPPSSPSVGWKPISDATPVLYAKLGPGKELYELHAGTESTPS 195

Qy 206 VVHVCDSDMEREEDPKTSPKPKINQTRPGLP 238
Db 196 VVHVCESETEEETK-NPKQKIAQTRRPDPB 227

RESULT 11
US-10-290-438-11
; Sequence 11, Application US/10290438
; Publication No. US20030186333A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; APPLICANT: Streeter, David G.
; TITLE OF INVENTION: DOWN SYNDROME CRITICAL REGION 1-LIKE PROTEIN
; FILE REFERENCE: PC-0013-1C1P
; CURRENT APPLICATION NUMBER: US/10/290, 438
; PRIORITY APPLICATION NUMBER: 09/614, 474
; PRIORITY FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO: 11
; LENGTH: 241
; SOFTWARE: PatentIn Ver. 2.1
; ORGANISM: Homo sapiens
; FEATURE: misc feature
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030186333A1 g6017919
; US-10-290-438-11

Query Match 54.7% Score 708.5; DB 14; Length 241;
Best Local Similarity 66.2%; Pred. No. 6.e-63; Mismatches 20; Gaps 2;

Qy 28 LCCIDRDAVTOCFA--EAFQALTDPSDLPNSLFA�CNVHSVPEEESEKSFEGLFRTY 85
Db 16 LSTDQEEEMIFGENDDDEMPSDLPNSLFA�CNVHSVPEEESEKSFEGLFRTY 75

Qy 86 DECYTFOLFKSFRVRINFSHPKSAARARIELHETQFRGKCLPLFYAQVOTPETDGDKLH 145
Db 76 DDQVTFOLFKSFRVRINFSKPEAAARARIELHETDNGQKLKLYPAQVOMSGEVRSKY 135

Qy 146 LAPPQAKQFLISPPSSPSVGWKPISDATPVLYAKLGPGKELYELHAGTESTPS 205
Db 136 LJPQPQPKQFLISPPSSPSVGWKPISDATPVLYAKLGPGKELYELHAGTESTPS 195

Qy 206 VVHVCDSDMEREEDPKTSPKPKINQTRPGLP 238
Db 196 VVHVCESETEEETK-NPKQKIAQTRRPDPB 227

RESULT 10
Query Match 54.7% Score 708.5; DB 9; Length 241;
Best Local Similarity 66.2%; Pred. No. 6.e-63; Mismatches 20; Gaps 2;

Qy 28 LCCIDRDAVTOCFA--EAFQALTDPSDLPNSLFA�CNVHSVPEEESEKSFEGLFRTY 85

RESULT 15
 US-09-782-953-12
 Sequence 12, Application US/09782953
 Patent No. US20020150953A1
 GENERAL INFORMATION
 APPLICANT: WILLIAMS, R. SANDERS
 APPLICANT: ROTHERMEL, BEVERLY
 TITLE OF INVENTION: CALCINEURIN INTERACTING PROTEIN (MCIP)
 FILE REFERENCE: UTSD:674.PZ1
 CURRENT APPLICATION NUMBER: US/09/782,953
 CURRENT FILING DATE: 2001-02-13
 PRIOR APPLICATION NUMBER: 60/216,601
 PRIOR FILING DATE: 2000-07-07
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 12
 LENGTH: 197
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-782-953-12

Query Match 47.5%; Score 616; DB 9; Length 197;
 Best Local Similarity 62.6%; Pred. No. 1.1e-33;
 Matches 117; Conservative 27; Mismatches 35; Indels 8; Gaps 2;
 Qy 57 NSLFACNTHOSVFEERESKEFEGLFRTYDECVTFOLFKSFRVRINFSHPKSAARARIE 116
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 11 SSSLIACTVANSDFSESETRAKFESLFRYDQITQYFKSFGRVRINFSNPFAADRLQ 70
 Qy 117 LHETQFRGKKLPLYFAQVQTPTEDGDKLHAPPQAKOFLISPPSSPSVGKPKISDATPV 176
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 71 LHKTIFLGKEMKLYFAOTLHIGSS---HLAPPNPDIQFLISPPASPPGVWKQVEPATPV 126
 Qy 177 LNYDLIYAVAKLGPGEKYLHAGTESTPSVVVHVCSMDREEDPKTS---PKPKINTQT 232
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 127 INYDLIYAVAKLGPGEKYLHAAATDTTPSVVHVVCBSSDQEEREEEMERMRPKPKIQT 186
 Qy 233 RRFGLPP 239
 |||:
 Db 187 RRPEYTP 193

Search completed: November 16, 2005, 16:53:29
 Job time: 124.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 16, 2005, 16:43:46 ; Search time 14:35 Seconds
(without alignments)
1567.977 Million cell updates/sec

Title: US-09-575-580B-5
Perfect score: 1296
Sequence: 1 EFVDPVRPRVRLQQASIP.....TSPKPKINOTRRPGLPPFGH 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

RESULT 1

T34305

hypothetical protein F54E7.7 - Caenorhabditis elegans

C.Species: Caenorhabditis elegans

C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T34305

R:Bentley, D.

A:Description: The sequence of C. elegans cosmid F54E7.

A:Reference number: 221502

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-239 <BEN>

A:Cross-references: UNIPROT:PS3806; EMBL:U00067; PIDN: AAC77519.1; GSPPDB: GN00021; CESPF

A:Experimental source: strain Bristol N2; clone F54E7

C:Genetics:

A:Gene: CESPF54E7.7

A:Map position: 3

A:Introns: 40/3; 7/8/2; 165/2; 205/1

Result No.	Score	Query Match	Length	DB ID	Description	Length
1	330.5	25.5	239	T34305	hypothetical protein nebula related protein	239
2	132	10.2	315	2 T49441	nebula related protein conserved hypothetical	315
3	99.5	7.7	163	2 S62444	cellulose-phospho	163
4	93.5	7.2	813	2 A72203	hypothetical protein	813
5	93	7.2	428	2 T32952	hypothetical protein	428
6	91.5	7.1	387	2 B84721	probable Poly-A Bi	387
7	91	7.0	671	2 C96534	protein CNK - frui	671
8	90.5	7.0	1557	2 T13160	hypothetical protein	1557
9	90	6.9	277	2 T37629	Mx protein - pig	277
10	88	6.8	160	2 C72206	gephyrin - rac	160
11	87.5	6.8	663	2 I46661	mannan endo-1,4-beta	663
12	87.5	6.8	736	2 JH0681	Bassoon protein -	736
13	86.5	6.7	1331	2 A48354	protein unc-22 limb	1331
14	86.5	6.7	3938	2 T42761	twitchin [similari	3938
15	86.5	6.7	6831	2 A88852	hypothetical protein	6831
16	86.5	6.7	6839	2 S57242	hypothetical protein	6839
17	86.5	6.7	7160	2 T27935	hypothetical protein	7160
18	86	6.6	885	2 A99353	hypothetical protein	885
19	86	6.6	885	2 B70393	hypothetical protein	885
20	86	6.6	2526	2 T20331	hypothetical protein	2526
21	85	6.6	454	2 A56354	yes-associated protein	454
22	85	6.6	698	2 JH0163	No-transient A	698
23	85	6.6	700	2 JH0162	No-transient A	700
24	84.5	6.5	457	2 S03361	Ig mu chain C regi	457
25	84.5	6.5	1106	1 PFRGCB	platelet-derived g	1106
26	83.5	6.4	1444	2 B84409	hypothetical protein	1444
27	83.5	6.4	3942	2 T42310	Bassoon protein -	3942
28	83	6.4	1098	1 PFMGRB	platelet-derived g	1098
29	82.5	6.4	1044	2 T1044	translation initia	1044

RESULT 2

T49641

nebula related protein [imported] - Neurospora crassa

C:Species: Neurospora crassa

C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004

C:Accession: T49641

R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Hartmann, B.; Holland, R.; Nyakatura

Submitted to the Protein Sequence Database, May 2000

A:Reference number: 225022

A:Accession: T49641

A:Source: preliminary

A:Molecule type: DNA

A:Residues: 1-315 <SCH>

A;Cross-references: UNIPROT:Q9PP59; EMBL:AL355932; GSPDB:GN00116; NCSP:BS022.230 A;Experimental source: BAC clone B5022; strain OR74A C;Genetics: A;Gene: NCSP:BS022.230 A;Map position: 6	Matches 51; Conservative 26; Mismatches 91; Indels 30; Gaps 6;	Matches 28; Conservative 13; Mismatches 29; Indels 13; Gaps 3;
Query Match Best Local Similarity 25.8%; Score 132; DB 2; Length 315; Pred. No. 0.00043;	Qy 51 DFSDLP-----NSIFACNVHQSVFEEESKEKPEGLFRTYDECUTFQLFKSPRVR 101 Db 48 DLSNLPLPSQPTPPSNTLIFTNTNSLOVSAONLTIRDLISOTAPIFAWSPLKSPRRII 107	Qy 146 LAPPQPKAFQFLSPJSPSSPSVQWKPSPDATP--VNNDLIVYAVAKLGPGKEYELDAGTES 202 Db 85 LQVPKFBNWLSPSSPPNWPVEESPNSQHILAHDIQLKLDDGNAALLNDHSAG-- 141
Matches 51; Conservative 26; Mismatches 91; Indels 30; Gaps 6;	Qy 203 TPSVYVHVCDSDMEREDPKTSP 225 Db 142 -PQIVI-----SERNNTKETSP 157	Qy 203 TPSVYVHVCDSDMEREDPKTSP 225 Db 142 -PQIVI-----SERNNTKETSP 157
RESULTS 4		
Qy 102 INFSHPKRAARIAELHTQFRKKLPYFAQVQTDFGDKHLAPPQPKFLSPPS 161 Db 108 VTFPDEQAAIAATRSVWDAAIGCRVYFGQTPIDVSAADKHLALPDAGKLFFFSPPP 167	Qy 102 INFSHPKRAARIAELHTQFRKKLPYFAQVQTDFGDKHLAPPQPKFLSPPS 161 Db 108 VTFPDEQAAIAATRSVWDAAIGCRVYFGQTPIDVSAADKHLALPDAGKLFFFSPPP 167	C;Species: Thermotoga maritima C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004 C;Accession: A72203
Qy 162 SPSVGKWD-ISA-TPVLYNDLILYAVAKLGPGKEYELHAGTESTPSVYVHVCDSMERE 218 Db 168 SPPHDWERMEDAPNTMWAEDLAELAKL-----REHHNNPNIGI----DADVK-- 211	Qy 162 SPSVGKWD-ISA-TPVLYNDLILYAVAKLGPGKEYELHAGTESTPSVYVHVCDSMERE 218 Db 168 SPPHDWERMEDAPNTMWAEDLAELAKL-----REHHNNPNIGI----DADVK-- 211	R;Neilson, K.E.; Clayton, R.A.; Gill, S.R.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Phillips, C.A.; Richardson, D., C.M.
Qy 219 EDPKTSPPKINOTRRPG 236 Db 212 --APVSPASDGCGSSSRPG 227	Qy 219 EDPKTSPPKINOTRRPG 236 Db 212 --APVSPASDGCGSSSRPG 227	Nature 399, 323-329, 1999 A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq. A;Reference number: A72200; PMID:93287316; PMID:10360571 A;Accession: A72203 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-113 <ARN> A;Cross-references: UNIPROT:Q9X2G3 ; GB:AE001822 ; GB:AE000512 ; NID:g4982429 ; PIDN:AAD3691 A;Experimental source: strain MSB8 C;Genetics:
RESULTS 3		
S62444 conserved hypothetical protein SPAC13G6.15C - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 C;Accession: S62444; S62549; T37650; T38331 R;Odeil, C.; Bowman, S. Submitted to the EMBL Data Library, October 1995 A;Reference number: S62444 A;Accession: S62444 A;Molecule type: DNA A;Residues: 1-163 <ODR> A;Cross-references: UNIPROT:Q09791; EMBL:Z54308; PIDN:CAA91108.1; PID:g1008985; R;Odeil, C.; Bowman, S.; Churcher, C.M.; submitted to the EMBL Data Library, November 1995 A;Reference number: S62546 A;Accession: S62549 A;Molecule type: DNA A;Residues: 1-163 <ODR> A;Cross-references: EMBL:267757; NID:g1061288; PIDN:CAA91769.1; PID:g1061292 R;Odeil, C.; Bowman, S.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V. Submitted to the EMBL Data Library, October 1995 A;Reference number: 221734 A;Accession: T37650 A;Molecule type: DNA A;Residues: 1-163 <ODR> A;Cross-references: EMBL:254308; PIDN:CAA91108.1; GSPDB:GN00066; SPDB:SPAC13G6.15C A;Experimental source: strain 972h; cosmid c13G6 R;Odeil, C.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. Submitted to the EMBL Data Library, November 1995 A;Reference number: 221786 A;Accession: T38331 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-163 <ODR> A;Cross-references: EMBL:267757; PIDN:CAA91769.1; GSPDB:GN00066; SPDB:SPAC24B11.04C A;Experimental source: strain 972h; cosmid c24B11 C;Genetics: A;Gene: SPAC24B11.04C; SPAC13G6.15C; SPAC24B11.04C	Query Match 7 / 2%; Score 93.5 ; DB 2 ; Length 813; Best Local Similarity 22 / 2%; Pred. No. 3-7; Matches 58; Conservative 40; Mismatches 112; Indels 51; Gaps 12;	
RESULTS 5		
T32952 hypothetical protein C15B6.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T32952 R;Rohlfing, T.; Biewald, T. Submitted to the EMBL Data Library, February 1998 A;Description: The sequence of C. elegans cosmid C15E6. A;Reference number: Z21253 A;Accession: T32952 A;Status: preliminary; translated from GB/ENBL/DDBJ A;Molecule type: DNA A;Residues: 1-428 <ROH> A;Cross-references: EMBL:AF045636; PIDN: AAC02559.1; GSPDB:GN00022; CESP:C15E6.1 A;Experimental source: strain Bristol N2; clone C15E6	Qy 2 FVDPRPRPRVRLQGQASIPED-GGFLFLCCICIDRD-WAVT-----QCFAEEAQFQALT 50 Db 47 YKDRDR-RITRTRNNVPTNVTAGGYFYIEENGDFWTPTWMPVKDLSFEARHGLGYT 105 Qy 51 DFSIDLNSL-----PACNYHQSYVPEEESEKEKPEGLFRTYDECUTFQL--FKSF 97 Db 106 KITGEINGLRATITYFVPRHETGEHYLVLENKAEXPKIKLFSTFPCFLWNALDDMTNF 165 Qy 98 RRVTRNFSHPKSAAARARIELHEFTQRGKPLKPLPVQQT-----ETDGDK-LHLLPQPA 152 Db 166 QR---NYSTGEVIEEGSVTHKTEFRRNHYAFTSVNOPIDGFDTRESFIGLYSGFEEA 222 Qy 153 KQFLI--SPPSSPSVQWKPISDATPVLYNDLILYAVAKLGPGKEYELHAGTESTPSVYVHV 210 Db 223 PQAIVGKPRNSVASWAPLASH-----YLETELAPSEKRL-----IFILGVY 266 Qy 211 CDSDMEREEDPKTSKPKINQ 231 Db 267 ENPEEKWKEKGIVNICKRAKE 287	

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C96534
C;Species: Arabidopsis thaliana
C;Location: Chr 1: 1870000..1870000
C;Map position: 4
A;Gene: C15B6.1
A;Map position: 4
A;Introns: 124/2; 196/3
Query Match 7.2%; Score 93; DB 2; Length 428;
Best Local Similarity 24.2%; Pred. No. 1.; Indels 62; Gaps 11;
Matches 52; Conservative 28; Mismatches 73; Indels 62; Gaps 11;
Oy 65 HQSVEEEESKE-KPEGLERT---YDVCVTQFLKSPRVRIN---FISHPKSAARARI 115
Db 168 HNPFDDEEEERSSQGCGTSDGPFDNSGSNENQLRKKLKEAHLUSSSSEI 227
Qy 116 ---ELHETQFRGKLPPLYAQVOTPETGDKLHLAPPQA-----KQFLISPPS 162
Db 228 VEASIHEDP-----PIWMAQI-----EKPCKRAIAFDNADFDNSPLH 271
Qy 163 P-----SVGMKRBISDATAFPLNVD-----ELHA 198
Db 272 HYSAVHLETLGLSPLLEAQRLANRARRHKPSNTSLAEAKLARORYSNASDIRREBEE 331
Qy 199 GTESTPSVYVHCDSDMREEDPKTSKPKINGTR 233
Db 332 VVEEDPAVNVPLRKDLIEVEAFKSVRPRYRKS 366
RESULT 6
B84721 hypothetical protein At2g31470 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayan, L.; Tallon, L.; eus, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-387 <STO>
A;Cross-references: UNIPROT:Q9SIC2; GB:AE002093; NID:94589954; PIDN:AAD26472.1; GSPDB:GN
C;Genetics:
A;Gene: Atcg31470
A;Map position: 2
C;Superfamily: Arabidopsis thaliana hypothetical protein At2g31470
Query Match 7.1%; Score 91.5; DB 2; Length 387;
Best Local Similarity 23.1%; Pred. No. 2.2; Indels 39; Gaps 8;
Matches 23; Conservative 25; Mismatches 79; Indels 39; Gaps 8;
Qy 30 CIDRDWAVTCFAEEAFAQALTDSDL-----PNSLIFACNTHQSVP-----EEESKE 76
Db 47 CVSKLWA-----STIRLPYPTELYLTKSARPRLLFACQKHRELFFSTPQPHNNE 98
Qy 77 KPEGFLRTYDECVTQFLPKSFRRVRFNFSPKSAARARIELHETQFRKLPFLYFAQVQT 136
Db 99 SSSPLAASPFMKIIPFD----GRFLNISP----IGGLVPRVREQLKGRTKTPBEVSALCN 149
Qy 137 PSTDGDKLHLAPPQPAKOFFLISPPSSPSVGWKPISDATPVLNYDLILYAVAKLGPGEKEYL 196
Db 150 EST-GQSLTRLPKBRTRKRIW---GTSHEGYDIEQFKVLSMNIGDVYK---EHVVL 200
Qy 197 HAGTES 202
Db 201 TLGTEN 206
RESULT 7
C96534 probable Poly-A Binding Protein [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana
C;Location: Chr 1: 1870000..1870000
C;Map position: 2
A;Gene: C15B6.1
A;Map position: 2
A;Introns: 124/2; 196/3
Query Match 7.0%; Score 90.5; DB 2; Length 1557;
Best Local Similarity 24.2%; Pred. No. 15; Mismatches 47; Conservative 22; Indels 49; Gaps 8;
Db 511 FDAEKDYV-MKNEKEPKICNVVENTILTPEPFPDADEDEDALTELTNCNKTAELLAIN 569

Qy 87 -----ECVTFOLFKSFRVRINFSHPKSAARARIELHET--QFRGKQLPLYFAQ 133
 Db 570 LATRGQDDPLAEAINMPHQGRGLPKSHETPAYNSGERSDTPPAIEPRK---EFLL 626
 Qy 134 VQTPTEDDKLHLAPPQAKOFLISPPSPSYGWKP1S---DATPVINYDLIYAV---AKL 188
 Db 627 VTPP-----APPRKOREMTTPAVPPPCKPASMQPASSITISIPVPPVPAV 678
 Qy 189 GPEEKYEHAGTES 202
 Db 679 DFSEISELHTPSKS 692

RESULT 9
 hypothetical protein SPAC13F5_04c - fission yeast (Schizosaccharomyces pombe)
 C;Species: Schizosaccharomyces pombe
 C;Accession: T37629
 R;Brown, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
 Submitted to the EMBL Data Library, September 1997
 A;Reference number: Z21733
 A;Accession: T37629
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-277 <BROW>
 A;Cross-references: UNIPROT:O13703; EMBL:Z99091; PIDN:CAB117671; GSPDB:GN00066; SPDB:SF
 C;Genetics:
 A;Gene: SPDB:SPAC13F5_04c
 A;Map position: 1
 A;Introns: 20/3

Query Match Score 6.9%; Best Local Similarity 22.9%; Length 277; Matches 46; Conservative 21; Mismatches 62; Indels 72; Gaps 8;

Qy 88 CTVTFOLFKSFRVRINP-----SHPKSAR-----ARIELHETQFRGK 125
 Db 2 CFFERFLVSFAFLRISPLSITKSIKEFKRLAQVANPQRKAKTPSNHATEFLQQQSNTN 61

Qy 126 KLPFLYPAQVQPTETDGDKLHLAPP---QPAOKOFLISPPSPSYGWKP---ISDA 173
 Db 627 TLPTQEAAVETNASASHETSFLPALTPSPAAASISIPTKSAVSSEENADVKSLSSTPA 121

Qy 174 TPVLVINYDLIYAVAKLGPGEKYE-----LHAGTESTPSVVHVCDSDMEREEDPKTSPK- 226
 Db 122 APQLN-----SPSHSYKEPTTFPSTISITENLPTI-----DPTRSTRS 158

Qy 227 -----PKINOTRRPGLPP 239
 Db 159 SSHIQSLSPESKQTSQDHRRP 179

RESULT 10
 C72706 hypothetical protein APE1066 - Aeropyrum pernix (strain K1)
 C;Species: Aeropyrum pernix
 C;Accession: C72706
 R;Kavarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahashi, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; DNA Res. 6, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
 A;Reference number: A72450; M0ID:99310339; PMID:10382966

RESULT 11
 C;Superfamily: Aeropyrum pernix hypothetical protein APE1066
 Query Match Score 6.8%; Best Local Similarity 31.5%; Matches 35; Conservative 8; Mismatches 26; Indels 42; Gaps 7;

Qy 141 GDKLHLAPPQAKOFLISPPSPSYGWKP1SDATPVINY-----DLIYAVAKLGP 190
 Db 11 GNLLVTHPPEAGQD-DGPP-----LTPVNNYNGVQLGVGDSLH---KQGP 54

Qy 191 GEKYELHAGTESTPSVYVHVCDSDMEREEDPKTSPKPINOTRRPGLPPFG 241
 Db 55 RE-YPLYRLTPKL-----CNPD-----SVFTNLQNLNTPGJPPAG 89

RESULT 11
 I46611
 Mx protein - pig
 C;Species: Sus scrofa domesticus (domestic pig)
 C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 C;Accession: I46611
 R;Mueller, M.; Winnacker, E.L.; Brem, G.
 J. Interferon Res. 12, 119-129, 1992
 A;Title: Molecular cloning of porcine Mx cDNAs: new members of a family of interferon-inducible genes
 A;Reference number: I46611; MUID:92251238; PMID:1578186
 A;Accession: I46611
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-663
 A;Cross-references: UNIPROT:P27594; GB:M65087; NID:9164591; PIDN:AAA11090.1; PID:gi164592
 C;Superfamily: dynamin-related protein VPS1

Query Match Score 6.8%; Best Local Similarity 23.9%; Pred. No. 9.6%; Matches 52; Conservative 34; Mismatches 63; Indels 69; Gaps 12;

Qy 17 ASIPED-GGGLFFLCCIDRDWAVTCQFCFAERAFAQALTDPSDLPNSUFACTVHQSVFEEEEE 74
 Db 363 SDIPEBESGRNPFGL-IDK-----SDI-----TALI_QGEEL 396

Qy 75 KEKFEGLFRYDECYTQFOLFKSFR-----VRINFSHPKSAARARIELHETQFRGK 126
 Db 397 VVEY-----EC-----RLPTKMRNEFCRMSAWVKNFKNGYDAICKQOLQFENQYGRG 445

Qy 127 LPLYFAQVQPTETDGDKLHLAPPQAKQFLISPPSPSYGWKP1SDATPVINYDLIYAVA 186
 Db 446 LP-GPNYKCFETILKKQVSYLEEAVDMLHTVLDLRAFTDVSET----NPN----- 494

Qy 187 KLGPGEKYLHAGTESTPSVYVHVCDSDMEREEDPKTS 224
 Db 495 -----EFFNLHRTAKS-----KTEDIKLDEQEKEAETS 521

RESULT 12
 JH0681
 gphyrin - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 12-Jul-2004
 C;Accession: JH0681; S24937
 R;Prior, P.; Schmidt, B.; Grenningloh, G.; Pribilla, I.; Beyreuther, K.; M. Neuron 8, 1161-1170, 1992
 A;Title: Primary structure and alternative splice variants of gphyrin, a putative glycoprotein
 A;Reference number: JH0681; MUID:92304983; PMID:1319186
 A;Accession: JH0681
 A;Molecule type: mRNA
 A;Residues: 1-736
 A;Cross-references: UNIPROT:003555; EML:CAA47009.1; PID:gi56312
 A;Experimental source: spinal cord
 C;Comment: This protein anchors the glycine receptor to subsynaptic microtubules.
 C;Superfamily: bifunctional molybdenum cofactor biosynthesis protein, Gphyrin type
 C;Keywords: cytoskeleton; phosphoprotein; transmembrane protein
 F;147, 151-222, 270-294, 371, 525, 697, 702/Binding site: phosphate (Ser) (covalent) #status p
 F;276, 286/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match Score 87.5; DB 2; Length 736; Best Local Similarity 21.5%; Pred. No. 11; Matches 57; Conservative 28; Mismatches 73; Indels 107; Gaps 10;	Db 313 -----GQWTKTNAIGTSSTPTP-----STVTPTPTPPTVTATPPTPTP 357
Qy 70 EEEESKEKEKGLPLRTYDCVTFOLFKSFRVRVINFSHPSAARARIELHETQFRG-KKLIP 128 Db 213 EEEEEEKKDSGVASTEDS-----SSSHITAAALARPKPDSIISRGVQVLP 257	RESULT 14 T42761 Bassoon protein - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004 R;Dieck, S.; Sammarit-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex J. Cell Biol. 142, 499-509, 1998 A;Title: Bassoon, a novel zinc-finger CGG/Glutamine-repeat protein selectively localized A;Reference number: Z222249; MUID:93345363; PMID:9679147 A;Accession: T42761 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-3938 <DIE> A;Cross-references: UNIPROT:088778; EMBL:Y16563; NID:93413503; PIDN:CAA76287_1; PID:g344 A;Experimental source: strain Sprague Dawley; brain C;Function: A;Description: may be involved in cytoskeletal organization at the site of neurotransmitt A;Note: Component of the presynaptic cytoskeleton C;Keywords: coiled coil; zinc finger
Qy 129 LYFAQVQTPETGDKLHLAP-----POPAKOFILIS----- 158 Db 258 RDTASLSTSPSSEPAQATSRSLASCTPKVOSRCSSRENILRASHSAVIDTKVARRHR 317	Query Match Score 6.7%; DB 2; Length 3938; Best Local Similarity 30.4%; Pred. No. 1.1e+02; Matches 34; Conservative 15; Mismatches 40; Indels 23; Gaps 7; C;Species: Caenorhabditis elegans C;Accession: B43745 R;Gibbs, M.D.; Saul, D.J.; Luthi, E.; Bergquist, P.L. Appl. Environ. Microbiol. 58, 3864-3867, 1992 A;Title: The beta-mannanase from "Caedocellum saccharolyticum" is part of a multidomain A;Reference number: A48954; MUID:93119139; PMID:1476429 A;Status: preliminary A;Molecule type: nucleic acid A;Residues: 1-131 <GIB> A;Cross-references: UNIPROT:P22533; GB:J01257; NID:9144290; PIDN:AAA71897_1; PID:g144291 A;Note: sequence extracted from NCBI backbone (NCBIN:121576; NCBI:121577) R;Luechi, E.; Bhana Jasmat, N.; Grayling, R.A.; Love, D.R.; Bergquist, P.L. Appl. Environ. Microbiol. 57, 694-700, 1991 A;Title: Cloning, sequence analysis, and expression in Escherichia coli of a gene coding A;Reference number: A43745; MUID:91247819; PMID:2039230 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-337, 'PRORQHQ'R, <LUE> A;Cross-references: EMBL:J36063; NID:g144292; PIDN:AAA72861_1; PID:g144294 A;Note: this sequence has been revised in reference A48954 C;Keywords: glycosidase; hydrolase; polysaccharide degradation
Qy 159 ---PPSSPSVGWMKPISDADTPVNYDIL-----YA 184 Db 318 MSFPLTSMDKAIFTVLEMTPVIGTEILNYRDGMGRVLAQDYVAKDNLUPFPASVKDGYA 377	Query Match Score 6.7%; DB 2; Length 3938; Best Local Similarity 30.4%; Pred. No. 1.1e+02; Matches 34; Conservative 15; Mismatches 40; Indels 23; Gaps 7; C;Species: Caenorhabditis elegans C;Accession: B43745 R;Gibbs, M.D.; Saul, D.J.; Luthi, E.; Bergquist, P.L. Appl. Environ. Microbiol. 58, 3864-3867, 1992 A;Title: The beta-mannanase from "Caedocellum saccharolyticum" is part of a multidomain A;Reference number: A48954; MUID:93119139; PMID:1476429 A;Status: preliminary A;Molecule type: nucleic acid A;Residues: 1-131 <GIB> A;Cross-references: UNIPROT:P22533; GB:J01257; NID:9144290; PIDN:AAA71897_1; PID:g144291 A;Note: sequence extracted from NCBI backbone (NCBIN:121576; NCBI:121577) R;Luechi, E.; Bhana Jasmat, N.; Grayling, R.A.; Love, D.R.; Bergquist, P.L. Appl. Environ. Microbiol. 57, 694-700, 1991 A;Title: Cloning, sequence analysis, and expression in Escherichia coli of a gene coding A;Reference number: A43745; MUID:91247819; PMID:2039230 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-337, 'PRORQHQ'R, <LUE> A;Cross-references: EMBL:J36063; NID:g144292; PIDN:AAA72861_1; PID:g144294 A;Note: this sequence has been revised in reference A48954 C;Keywords: glycosidase; hydrolase; polysaccharide degradation
Qy 185 V-AKLGPEKY --ELHAGTESTPSV-----VYVCDSDMERED 220 Db 378 VRAADGPDRFLIGESQAGEQPTQTVMPQQVMRVTGAPIPGCADAVVQVEDTBLLRESD 437	Query Match Score 6.7%; DB 2; Length 3938; Best Local Similarity 30.4%; Pred. No. 1.1e+02; Matches 34; Conservative 15; Mismatches 40; Indels 23; Gaps 7; C;Species: Caenorhabditis elegans C;Accession: B43745 R;Gibbs, M.D.; Saul, D.J.; Luthi, E.; Bergquist, P.L. Appl. Environ. Microbiol. 58, 3864-3867, 1992 A;Title: The beta-mannanase from "Caedocellum saccharolyticum" is part of a multidomain A;Reference number: A48954; MUID:93119139; PMID:1476429 A;Status: preliminary A;Molecule type: nucleic acid A;Residues: 1-131 <GIB> A;Cross-references: UNIPROT:P22533; GB:J01257; NID:9144290; PIDN:AAA71897_1; PID:g144291 A;Note: sequence extracted from NCBI backbone (NCBIN:121576; NCBI:121577) R;Luechi, E.; Bhana Jasmat, N.; Grayling, R.A.; Love, D.R.; Bergquist, P.L. Appl. Environ. Microbiol. 57, 694-700, 1991 A;Title: Cloning, sequence analysis, and expression in Escherichia coli of a gene coding A;Reference number: A43745; MUID:91247819; PMID:2039230 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-337, 'PRORQHQ'R, <LUE> A;Cross-references: EMBL:J36063; NID:g144292; PIDN:AAA72861_1; PID:g144294 A;Note: this sequence has been revised in reference A48954 C;Keywords: glycosidase; hydrolase; polysaccharide degradation
Qy 221 PKTSP-KPKINQTRRPG--LPPFGH 242 Db 438 DGTEELEFLTRILYQARPQGDIDRPGH 462	Query Match Score 6.7%; DB 2; Length 3938; Best Local Similarity 30.4%; Pred. No. 1.1e+02; Matches 34; Conservative 15; Mismatches 40; Indels 23; Gaps 7; C;Species: Caenorhabditis elegans C;Accession: B43745 R;Gibbs, M.D.; Saul, D.J.; Luthi, E.; Bergquist, P.L. Appl. Environ. Microbiol. 58, 3864-3867, 1992 A;Title: The beta-mannanase from "Caedocellum saccharolyticum" is part of a multidomain A;Reference number: A48954; MUID:93119139; PMID:1476429 A;Status: preliminary A;Molecule type: nucleic acid A;Residues: 1-131 <GIB> A;Cross-references: UNIPROT:P22533; GB:J01257; NID:9144290; PIDN:AAA71897_1; PID:g144291 A;Note: sequence extracted from NCBI backbone (NCBIN:121576; NCBI:121577) R;Luechi, E.; Bhana Jasmat, N.; Grayling, R.A.; Love, D.R.; Bergquist, P.L. Appl. Environ. Microbiol. 57, 694-700, 1991 A;Title: Cloning, sequence analysis, and expression in Escherichia coli of a gene coding A;Reference number: A43745; MUID:91247819; PMID:2039230 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-337, 'PRORQHQ'R, <LUE> A;Cross-references: EMBL:J36063; NID:g144292; PIDN:AAA72861_1; PID:g144294 A;Note: this sequence has been revised in reference A48954 C;Keywords: glycosidase; hydrolase; polysaccharide degradation
Qy 221 ---DGLGLFLCCID----RDWAVTOCAFEEAFQALTDPSLNSIFACNYHSQEEEESKE 76 Db 185 DAGKHTIMVDAWNQGDWNNTM--RDNAQSIMEADPLRNLYFSIAMY----- 230	Query Match Score 6.7%; DB 2; Length 3938; Best Local Similarity 30.4%; Pred. No. 1.1e+02; Matches 34; Conservative 15; Mismatches 40; Indels 23; Gaps 7; C;Species: Caenorhabditis elegans C;Accession: B43745 R;Gibbs, M.D.; Saul, D.J.; Luthi, E.; Bergquist, P.L. Appl. Environ. Microbiol. 58, 3864-3867, 1992 A;Title: Cloning, sequence analysis, and expression in Escherichia coli of a gene coding A;Reference number: A43745; MUID:91247819; PMID:2039230 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-337, 'PRORQHQ'R, <LUE> A;Cross-references: EMBL:J36063; NID:g144292; PIDN:AAA72861_1; PID:g144294 A;Note: this sequence has been revised in reference A48954 C;Keywords: glycosidase; hydrolase; polysaccharide degradation
Qy 77 KPEGLFRPYDECVTFOLFKSFRVRVINFSHPSKAARARIELHETQFRGKKLPLYFAQVQT 136 Db 231 ---GVNT-----ASKVVEYIKSFVDQGLPVIGERGH 260	Query Match Score 6.7%; DB 2; Length 3938; Best Local Similarity 30.4%; Pred. No. 1.1e+02; Matches 34; Conservative 15; Mismatches 40; Indels 23; Gaps 7; C;Species: Caenorhabditis elegans C;Accession: B43745 R;Gibbs, M.D.; Saul, D.J.; Luthi, E.; Bergquist, P.L. Appl. Environ. Microbiol. 58, 3864-3867, 1992 A;Title: Cloning, sequence analysis, and expression in Escherichia coli of a gene coding A;Reference number: A43745; MUID:91247819; PMID:2039230 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-337, 'PRORQHQ'R, <LUE> A;Cross-references: EMBL:J36063; NID:g144292; PIDN:AAA72861_1; PID:g144294 A;Note: this sequence has been revised in reference A48954 C;Keywords: glycosidase; hydrolase; polysaccharide degradation
Qy 137 PETDGKHLAPPOAKOFILISPPS-----SPSVG-----WKPISDADTPVNYDILY 183 Db 261 QHTDGDPEEAIVRYAQKXQKIGLFSWWSGNSSYVGYLDMVNWNWP--NNPTPN----- 312	Query Match Score 6.7%; DB 2; Length 3938; Best Local Similarity 30.4%; Pred. No. 1.1e+02; Matches 34; Conservative 15; Mismatches 40; Indels 23; Gaps 7; C;Species: Caenorhabditis elegans C;Accession: B43745 R;Gibbs, M.D.; Saul, D.J.; Luthi, E.; Bergquist, P.L. Appl. Environ. Microbiol. 58, 3864-3867, 1992 A;Title: Cloning, sequence analysis, and expression in Escherichia coli of a gene coding A;Reference number: A43745; MUID:91247819; PMID:2039230 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-337, 'PRORQHQ'R, <LUE> A;Cross-references: EMBL:J36063; NID:g144292; PIDN:AAA72861_1; PID:g144294 A;Note: this sequence has been revised in reference A48954 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Qy	1.27	LPL-----	-YFAVQQTPTEDG-----	-DLKLHIAOPPAKQFLISP-----	-PSSP 163
:	:	:	:	:	:
Db	3.964	VPVSAFVTGTISITVKLTGEHEYFRYMAENTFGRSISLNNTDBPVLA	KDGPFGKPGRP	4 023	
Qy	1.64	-----SVGWKPDTS-----	-ATPVLYNVDL-----	-----	181
:	:	:	:	:	
Db	4.024	BIVDTNDHDIKWDDPRDNGGSPVHDYIERKDA	KTGRIWKVNTPVQGTAFSDTRVQK	4 083	
Qy	1.82	-----LYAVAKLGGEKYELHAGTESTPSVYHVCDSDMERE-----	-DP-----	-----	221
:	:	:	:	:	
Db	4.084	GHTYEYRVAVNKGCPQSDSSAAATAKPMHEA	KPDLDLGKEFRVKAGEPLVITIPF	4 143	
Qy	2.22	KTSPRKIEINQTRRPGPPFG	241		
:	:	:	:	:	
Db	4.144	TASPOIDISWKEGGPLAG	4 163		

Search completed: November 16, 2005, 17:13:07
Search time : 15.85 sec

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OM protein - protein search, using SW model

Run on: November 16, 2005, 16:32:05 ; Search time 60.5 Seconds
 (without alignments)
 2048.317 Million cell updates/sec

Title: US-09-575-580B-5

Perfect score: 1296

Sequence: 1 EFVDPVRVRPVRLLQQASIP.....TSPRKPKINQTRRPGLPPFGH 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:

1612378

Description: 1612378

Score Match Length DB ID

Result No.	Score	Match	Length	DB	ID
1	1186	91.5	243	2	Q8VIP4
2	1176	90.7	243	2	Q8CH26
3	1116	86.1	243	2	Q8N116
4	882	68.1	197	1	CCP2_MOUSE
5	876	67.6	197	2	Q8CH27
6	868	67.0	192	2	Q8VIP5
7	861	66.4	225	2	Q8EJ0
8	848	65.4	197	1	CCP2_HUMAN
9	729	55.9	195	2	Q6NSN4
10	720.5	55.6	239	1	CCP3_MOUSE
11	708.5	54.7	241	2	CCP1_HUMAN
12	702	54.2	230	2	Q6D639
13	648	50.0	252	2	Q7Z555
14	632	48.8	251	2	Q7INY3
15	617	47.6	197	1	CCP1_CRICR
16	616	47.5	197	1	CCP1_HUMAN
17	616	47.5	199	2	Q6IN33
18	615	47.5	197	2	Q6XXM7
19	614	47.4	199	2	Q8K4S2
20	608.5	47.0	198	1	CCPL_MOUSE
21	589	45.4	199	2	OTT0U1
22	588	45.4	199	2	Q6DK90
23	582	44.9	242	2	Q6ZB03
24	579	44.7	231	2	Q72XP4
25	540	41.7	196	2	Q6GCB1
26	522.5	40.3	210	2	Q6DC33
27	418.5	32.3	292	1	SRA_DROME
28	330.5	25.5	207	1	CCPE_CAEEL
29	132	10.2	315	2	Q9PS59
30	128.5	9.4	249	2	Q667G0
31	116.5	9.0	249	2	Q9P4A1

RESULT 1

Q8VIP4

Preliminary;

PRT; 243 AA.

ID Q8VIP4;

AC

Created)

DT 01-MAR-2002 (TrEMBLrel.

DT 01-MAR-2002 (TrEMBLrel.

Last sequence update)

DT 01-OCT-2003 (TrEMBLrel.

25, Last annotation update)

DE

Calcineurin inhibitor

protein ZAKI-4 beta.

GN

Name=Oscr11;

Synonyms=ZAKI-4 beta;

OS

Mus musculus (Mouse)

OC

Mammalia; Eukaryota;

Chordata;

Craniata;

Vertebrata;

Euteleostomi;

Muridae; Murinae; Mus.

RN [1]

SEQUENCE FROM N.A.

RA Kanou Y., Miyazaki T., Seo H., Murata Y.;

RL Submitted (MAY-2001) to the EMBL/GenBank/DDJB databases.

DR EMBL; AB61525; BAB71956.1;

DR MGD; MGJ:1858219; Descr1.

DR GO: GO_0019722; P:calcium-mediated signaling; IEA.

DR Pfam; PF04847; Calcipressin, 1.

SQ SEQUENCE 243 AA; 27332 MW; 2CDC8CJA810291851 CRC64;

Query Match 91.5% ; Score 1186; DB 2;

Best Local Similarity 98.2% ; Pred. No. 8-93;

Matches 223; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

SQ SEQUENCE 243 AA; 27332 MW;

PRT; 243 AA.

RESULTS 2

Q8CH26

Preliminary;

PRT; 243 AA.

ID Q8CH26;

AC

Created)

DT 01-MAR-2003 (TrEMBLrel.

23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel.

25, Last annotation update)

DE ZAKI-4 beta.

DR Q9PS59

Neurospora

Q667G0

Cryptococcus

Q9P4A1

Cryptococcus

Q6C6F1

Yarrowia lae-

schiosacch-

Q9b19

mus musculu-

Q8K212

mus musculu-

Q9h2ns

homo sapien

Q9eh31

homo sapien

Q8bt12

debatyomyce

Q74zs6

ashbya goss

Q05030

ratetus norv-

Q9m6e4

nicotiana c

Q9fga3

arabidopsis

Q6z050

oryza sati-

Q6cmz1

kluyveromyces

Q8g7y8

bifidobacte-

OC	Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN/Strain; TISSUE=Brain;		
RA	Miyazaki T., Cao X., Kambe F., Ohmori S., Seo H.; Submitted (Dec-2001) to the EMBL/GenBank/DDBJ databases.		
RL	EMBL: AF45023; AAO15541.1;		
DR	GO; GO:0015722; P:calcium-mediated signaling; IEA.		
DR	InterPro; IPR006931; Calciipressin; 1.		
DR	Pfam; PF04847; Calciipressin; 1.		
SQ	SEQUENCE 243 AA; 27311 MW; 00B5BD1DCD0492D CRC64;		
Query Match	Score 90.7%; Score 1176; DB 2; Length 243;		
Best Local Similarity	96.5%;		
Matches	Pred. No. 6.2e-52;		
219; Conservative	4; Mismatches 0; Indels 0; Gaps 0;		
Db	13 LGQQASPEDGGFLFLCCIDRDWAVTQCPAAFAFOALTDPSDLPLNSLFAACNVHQSYFEEE 72		
Qy	73 ESKEKFFGGLFRYDECYTFQLFKSFRVRVIRNFSPHKSAAARARIELHETOPFRGKKLPLYFA 132		
Db	73 ESKEKFFGGLFRYDECYTFQLFKSFRVRVIRNFSPHKAARARARIELHETQFRGKKLPLYFA 132		
Qy	133 QVQTPEFDGDKLHLAPPOAKOFLISPPSSPVGKPIISDATPVLNYDLYYAVAKLGPGE 192		
Db	133 QVQTPEFDGDKLHLAPPOAKOFLISPPSSPVGKPIISDATPVLNYDLYYAVAKLGPGE 192		
Qy	193 KYELHACTESTPSVWVFCDSMEREEDPKTSPKPKINQTRPGLPP 239		
Db	193 KYELHACTESTPSVWVFCDSPLSLEEEDPKTSPKPKIOTRPGGLPP 239		
RESULT 3	SEQUENCE FROM N.A.		
Q8N116	PRELIMINARY; PRT; 243 AA.		
ID	Q8N116		
AC			
DT	01-OCT-2002 (T=EMBLres. 22; Created)		
DT	01-OCT-2002 (T=EMBLres. 22; Last sequence update)		
DE	Calciineurin inhibitor ZAK1-4 beta splice variant 1 (Calciineurin inhibitor ZAK1-4 beta splice variant 2).		
DB	Homo sapiens (Human)		
OS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
RN	[1] _TAXID=9606;		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RA	MEIDLINE=22250686; PubMed=12120666; DOI=10.1042/BJ20011797; Cao X., Miyazaki T., Sarkar D., Ohmori S., Seo H.; "Novel human ZAK1-4 isoforms: hormonal and tissue-specific regulation and function as calcineurin inhibitors.";		
RT	DR Biochem. J. 367:459-466 (2002).		
RT	DR EMBL:AY034085; AAK9806.1; -.		
RT	DR GO; GO:0015722; P:calcium-mediated signaling; IEA.		
RT	DR InterPro; IPR006931; Calciipressin.		
DR	Pfam; PF04847; Calciipressin; 1.		
SQ	SEQUENCE 243 AA; 27247 MW; 780073AB29A973E4 CRC64;		
Query Match	Score 86.1%; Score 1116; DB 2; Length 243;		
Best Local Similarity	91.6%;		
Matches	Pred. No. 7.9e-67;		
207; Conservative	9; Mismatches 10; Indels 0; Gaps 0;		
Db	14 GQQASPEDGGFLFLCCIDRDWAVTQCPAAFAFOALTDPSDLPLNSLFAACNVHQSYFEEE 73		
Qy	14 GQQHYPEDGGFLFLCCIDRDWAVTQCPAAFAFOALTDPSDLPLNSLFAACNVHQSYFEEE 73		
Db	14 SKEKFFGGLFRYDECYTFQLFKSFRVRINFSPHKSAAARARIELHETOPFRGKKLPLYFAQ 133		
Qy	74 SKEKFFGGLFRYDECYTFQLFKSFRVRINFSPHKSAAARARIELHETOPFRGKKLPLYFAQ 133		
Db	74 SKEKFFGGLFRYDDCVTFQLFKSFRVRINFSPNPKSAARARIELHETOPFRGKKLPLYFAQ 133		

RESULTS FROM N.A.
 STRAIN=BALB/C; TISSUE=Brain;
 MEDLINE=20187510; PubMed=10722714; DOI=10.1074/jbc.275.12.8719;
 Rothermel B., Vega R.B., Yang J., Wu H., Bassel-Duby R., Williams R.S.; "A protein encoded within the Down syndrome critical region is enriched in striated muscles and inhibits calcineurin signaling.";
 RT [2] J. Biol. Chem. 275:8719-8725(2000).
 RN [2]
 RP
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Brain;
 RX MEDLINE=20534793; PubMed=11080588; DOI=10.1016/S0378-1119(00)00407-8;
 RA Strippoli P., Petrucci M., Lenzi L., Carinci P., Zannotti M.; RT "The murine DESCR1-like 'Down syndrome Candidate region 1' gene family: conserved synteny with the human orthologous genes.";
 RA Gene 257:223-232(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=124603899;
 RA Straubberg R.L., Feingold B.A., Grouse L.H., Dege J.C., Schuler G.D., Klaunuer R.D., Collins F.S., Wagner L., Shemer C.M., Bhat N.K., Altenschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Hsieh F., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Bonaldo M.F., Stapleton M., Soares M.B., Brownstein M.J., Uedin T.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedin T.P., Toshimura S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullah S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley P.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahay J., Hellon E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.E., Jones S.J.M., Marrs M.A.; RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL CC -!- FUNCTION: Inhibits calcineurin-dependent responses by binding to the catalytic domain of calcineurin A. Could play a role during central nervous system development.
 CC -!- TISSUE SPECIFICITY: Highest expression in heart, skeletal muscle and brain. Lower expression in all other tissues.
 CC -!- SIMILARITY: Belongs to the DSER1 family
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.ebi.ac.uk/announce/> or send an email to license@ebi.ac.uk).

CC EMBL: AP237791; AAF63487_1; -;
CC EMBL: AP237887; AAF62538_1; -;
CC EMBL: BC049056; AAH49056_1; -;
DR MGD; MGID: 1858219; Dscr11; -;
DR InterPro: IPRO006931; Calcipressin.
Pfam: PF04847; Calcipressin_1.
SEQUENCE 197 AA; 22025 MW; CB1306B7B03E70F1 CRC64;

Query Match Score 832; DB 1; Length 197;
Best Local Similarity 91.8%; Pred. No. 4.9e-67;
Matches 168; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

Qy 57 NSLPACNTHQSVPFEEEEEKEKFGKLFLRYYDECYTFOLFKSFRVRINSHPKSAARARIE 116
DB 11 STLVACVVDVEVFPTNQEYKEKFGKLFLRYYDECYTFOLFKSFRVRINSHPKSAARARIE 70
Qy 117 LHETQFRGKFLPLPFAQVQTPTEDGDKHLAPPQAKOFLISPPSPVGWKPISDATPV 176
DB 71 LHETQFRGKFLPLPFAQVQTPTEDGDKHLAPPQAKOFLISPPSPVGWKPISDATPV 130
Qy 177 LNDLLYAVAKLGPGKELHAGTESTSVVVHVCDSMERMEDDPKTSPKPKINQTRPG 236
DB 131 LNDLLYAVAKLGPGKELHAGTESTSVVVHVCDSMERMEDDPKTSPKPKINQTRPG 190
Qy 237 LPP 239
DB 191 LPP 193

RESULT 5
Q8CH27 PRELIMINARY; PRT; 197 AA.
AC Q8CH27_1; -;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE ZAKI-4 alpha.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nistar; TISSUE=Brain;
RA Miyauchi T., Cao X., Kambe F., Ohmori S., Seo H.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AA459022; AA015540_1; -;
GO; GO:0019729; P:calcium-mediated signaling; IEA.
DR InterPro; IPR006331; Calcipressin.
Pfam; PF04847; Calcipressin_1.
SEQUENCE 197 AA; 21991 MW; D8C903B7A746F4B CRC64;

Query Match Score 876; DB 2; Length 197;
Best Local Similarity 90.7%; Pred. No. 1.6e-66;
Matches 166; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy 57 NSLPACNTHQSVPFEEEEEKEKFGKLFLRYYDECYTFOLFKSFRVRINSHPKSAARARIE 116
DB 11 STLVACVVDVEVFPTNQEYKEKFGKLFLRYYDECYTFOLFKSFRVRINSHPKSAARARIE 70
Qy 117 LHETQFRGKFLPLPFAQVQTPTEDGDKHLAPPQAKOFLISPPSPVGWKPISDATPV 176
DB 71 LHETQFRGKFLPLPFAQVQTPTEDGDKHLAPPQAKOFLISPPSPVGWKPISDATPV 130
Qy 177 LNDLLYAVAKLGPGKELHAGTESTSVVVHVCDSMERMEDDPKTSPKPKINQTRPG 236

CC or send an email to license@ebi.ac.uk.	Db 131 LNDLLYAVAKLGPGKELHAGTESTSVVVHVCDSMERMEDDPKTSPKPKINQTRPG 190
CC modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.ebi.ac.uk/announce/ or send an email to license@ebi.ac.uk.)	Qy 237 LPP 239
CC	Db 191 LPP 193
CC	RESULT 6 Q8VIPS PRELIMINARY; PRT; 192 AA. ID Q8VIPS AC Q8VIPS_1; -; DT 01-MAR-2002 (TREMBLrel. 20, Created) DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update) DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
CC	DE Calcineurin inhibitor protein ZAKI-4. GN Name=Dscr11; Synonyms=ZAKI-4; OS Mus musculus (Mouse) OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090; RN [1] RP SEQUENCE FROM N.A. RA Miyauchi T., Seo H., Murata Y.; RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases. DR EMBL; AB061524; BAB71955_1; DR MGI; MGI:1858219; Dscr11. DR GO; GO:0019722; P:calcium-mediated signaling; IEA. DR Pfam; PF04847; Calcipressin_1. SQ SEQUENCE 192 AA; 21540 MW; B2DB819FB36AB3 CRC64;
CC	Query Match Score 868; DB 2; Length 192; Best Local Similarity 90.2%; Pred. No. 7.3e-66; Matches 165; Conservative 4; Mismatches 14; Indels 0; Gaps 0; Qy 57 NSLPACNTHQSVPFEEEEEKEKFGKLFLRYYDECYTFOLFKSFRVRINSHPKSAARARIE 116 DB 6 STLVACVVDVEVFPTNQEYKEKFGKLFLRYYDECYTFOLFKSFRVRINSHPKSAARARIE 65 Qy 117 LHETQFRGKFLPLPFAQVQTPTEDGDKHLAPPQAKOFLISPPSPVGWKPISDATPV 176 DB 66 LHETQFRGKFLPLPFAQVQTPTEDGDKHLAPPQAKOFLISPPSPVGWKPISDATPV 125 Qy 177 LNDLLYAVAKLGPGKELHAGTESTSVVVHVCDSMERMEDDPKTSPKPKINQTRPG 236 DB 126 LNDLLYAVAKLGPGKELHAGTESTSVVVHVCDSMERMEDDPKTSPKPKINQTRPG 185 Qy 237 LPP 239 DB 186 LPP 188
CC	RESULT 7 Q86YJ0 PRELIMINARY; PRT; 225 AA. ID Q86YJ0 AC Q86YJ0_1; -; DT 01-JUN-2003 (TREMBLrel. 24, Created) DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update) DE DSCR11 protein. OS Homo sapiens (Human) OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; RN [1] RP SEQUENCE FROM N.A. RC TISSUE=Brain; RA Peingold B.A., Grouse L.H., Derge J.G., Schuler G.D., MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; RA Klausner R.D., Peingold B.A., Grouse L.H., Derge J.G., Schuler G.D., Altenschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.M., Shennan D., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Haieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Garcia A.M., Gay L.J., Hulyk S.W., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Pahey J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A., RA Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., RA Krzywinski M.C., Grimwood J., Myers R.M., Butterfield Y.S., RA GO; GO:00019722; RAH38509; P:calcium-mediated signaling; IEA. RA DR InterPro; IPR006331; Calcipressin; 1. RA PFam; PF04847; Calcipressin; 1. RA SEQUENCE 225 AA; 25075 MW; E56B705D3CE1E3B9 CRC64;	Query Match 66.4%; Score 861; DB 2i; Length 225; Best Local Similarity 99.1%; Pred. No. 3.5e-65; Matches 163; Conservative 8; Mismatches 12; Indels 0; Gaps 0; Qy 57 NSLFACNTHQSYPEEEEEEKEKEPEGLFPTYDECUTFQLFKSFRVRINSHPKSAARIE 116 Db 11 STLVACVVDVEFTENQEVKEKEPEGLFPTYDDCTVFQLFKSFRVRINSNPKSAARIE 70 Qy 117 LHETQFRGKKLPLHYAQVOTPBTGDKLHLAPPQAKQFLISPPSSPSVGKPKISDATPV 176 Db 71 LHETQFRGKKLHYAQVOTPBTGDKLHLAPPQAKQFLISPPSSPSVGKPKISDATPV 130 Qy 177 LNNDLLYAVAKLGPGEKVELHAGTESTPSVYVHCDSDMREEDPKTSPEKINKNOTRPG 236 Db 131 LNNDLLYAVAKLGPGEKVELHAGTESTPSVYVHCDSDIBBEDPKTSPEKINKNOTRPG 190 Qy 237 LPP 239 Db 191 LPP 193	RESULT 9 Q6NSN4 ID Q6NSN4 PRELIMINARY; PRT; 195 AA.
RN SEQUENCE FROM N.A. RC TISSUE:Kidney; PMID=12477932; DOI=10.1073/pnas.242603899; RX MEDLINE=22388257; PubMed=866294; DOI=10.1074/jbc.271.24.14567; RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., RA Altzschuler S.F., Zeeberg B.H., Bustein K.H., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Bosak S.A., McIwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	RESULT 8 CCP2_HUMAN ID CCP2_HUMAN STANDARD; PRT; 197 AA. AC Q142056 DT 30-MAY-2000 (Re) 39 Created DT 16-OCT-2001 (Re) 40 Last sequence update) DT 05-JUL-2004 (Re) 44 Last annotation update) DE Calcipressin 2 (Thyroid hormone-responsive protein ZAKI-4) (Down syndrome candidate region 1-like 1) (Myocyte-enriched calcineurin interacting protein 2) (MCIP2). DB Name=DSCR1; Synonyms=ZAK14; OS Homo sapiens (Human). OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Metazoa; Chordata; Craniata; Catarrhini; Hominidae; Homo. OC NCBI_TaxID=9606; RN SEQUENCE FROM N.A. RC TISSUE:Kidney; PMID=12477932; DOI=10.1073/pnas.242603899; RX MEDLINE=22388257; PubMed=866294; DOI=10.1074/jbc.271.24.14567; RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., RA Altzschuler S.F., Zeeberg B.H., Bustein K.H., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Bosak S.A., McIwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	RESULT 8 CCP2_HUMAN ID CCP2_HUMAN STANDARD; PRT; 197 AA. AC Q142056 DT 30-MAY-2000 (Re) 39 Created DT 16-OCT-2001 (Re) 40 Last sequence update) DT 05-JUL-2004 (Re) 44 Last annotation update) DE Calcipressin 2 (Thyroid hormone-responsive protein ZAKI-4) (Down syndrome candidate region 1-like 1) (Myocyte-enriched calcineurin interacting protein 2) (MCIP2). DB Name=DSCR1; Synonyms=ZAK14; OS Homo sapiens (Human). OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Metazoa; Chordata; Craniata; Catarrhini; Hominidae; Homo. OC NCBI_TaxID=9606; RN SEQUENCE FROM N.A. RC TISSUE:Kidney; PMID=12477932; DOI=10.1073/pnas.242603899; RX MEDLINE=22388257; PubMed=866294; DOI=10.1074/jbc.271.24.14567; RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., RA Altzschuler S.F., Zeeberg B.H., Bustein K.H., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Bosak S.A., McIwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA TISSUE:Brain; STRAUSBERG R.; Submitted (Oct-2002) to the EMBL/GenBank/DDBJ databases. DR EMBL; EC038509; RAH38509; P:calcium-mediated signaling; IEA. DR GO; GO:00019722; RAH38509; P:calcium-mediated signaling; IEA. DR InterPro; IPR006331; Calcipressin. DR Pfam; PF04847; Calcipressin; 1. DR SEQUENCE 225 AA; 25075 MW; E56B705D3CE1E3B9 CRC64;	Query Match 65.4%; Score 848; DB 1; Length 197; Best Local Similarity 88.0%; Pred. No. 3.8e-64; Matches 161; Conservative 8; Mismatches 14; Indels 0; Gaps 0; Qy 57 NSLFACNTHQSYPEEEEEEKEKEPEGLFPTYDECUTFQLFKSFRVRINSHPKSAARIE 116 Db 11 STLVACVVDVEFTENQEVKEKEPEGLFPTYDDCTVFQLFKSFRVRINSNPKSAARIE 70 Qy 117 LHETQFRGKKLPLHYAQVOTPBTGDKLHLAPPQAKQFLISPPSSPSVGKPKISDATPV 176 Db 71 LHETQFRGKKLHYAQVOTPBTGDKLHLAPPQAKQFLISPPSSPSVGKPKISDATPV 130 Qy 177 LNNDLLYAVAKLGPGEKVELHAGTESTPSVYVHCDSDMREEDPKTSPEKINKNOTRPG 236 Db 131 LNNDLLYAVAKLGPGEKVELHAGTESTPSVYVHCDSDIBBEDPKTSPEKINKNOTRPG 190 Qy 237 LPP 239 Db 191 LPP 193	RESULT 9 Q6NSN4 ID Q6NSN4 PRELIMINARY; PRT; 195 AA.
RA TISSUE:Brain; STRAUSBERG R.; Submitted (Oct-2002) to the EMBL/GenBank/DDBJ databases. DR EMBL; EC038509; RAH38509; P:calcium-mediated signaling; IEA. DR GO; GO:00019722; RAH38509; P:calcium-mediated signaling; IEA. DR InterPro; IPR006331; Calcipressin. DR Pfam; PF04847; Calcipressin; 1. DR SEQUENCE 225 AA; 25075 MW; E56B705D3CE1E3B9 CRC64;	Query Match 65.4%; Score 848; DB 1; Length 197; Best Local Similarity 88.0%; Pred. No. 3.8e-64; Matches 161; Conservative 8; Mismatches 14; Indels 0; Gaps 0; Qy 57 NSLFACNTHQSYPEEEEEEKEKEPEGLFPTYDECUTFQLFKSFRVRINSHPKSAARIE 116 Db 11 STLVACVVDVEFTENQEVKEKEPEGLFPTYDDCTVFQLFKSFRVRINSNPKSAARIE 70 Qy 117 LHETQFRGKKLPLHYAQVOTPBTGDKLHLAPPQAKQFLISPPSSPSVGKPKISDATPV 176 Db 71 LHETQFRGKKLHYAQVOTPBTGDKLHLAPPQAKQFLISPPSSPSVGKPKISDATPV 130 Qy 177 LNNDLLYAVAKLGPGEKVELHAGTESTPSVYVHCDSDMREEDPKTSPEKINKNOTRPG 236 Db 131 LNNDLLYAVAKLGPGEKVELHAGTESTPSVYVHCDSDIBBEDPKTSPEKINKNOTRPG 190 Qy 237 LPP 239 Db 191 LPP 193	RESULT 9 Q6NSN4 ID Q6NSN4 PRELIMINARY; PRT; 195 AA.
RA TISSUE:Brain; STRAUSBERG R.; Submitted (Oct-2002) to the EMBL/GenBank/DDBJ databases. DR EMBL; EC038509; RAH38509; P:calcium-mediated signaling; IEA. DR GO; GO:00019722; RAH38509; P:calcium-mediated signaling; IEA. DR InterPro; IPR006331; Calcipressin. DR Pfam; PF04847; Calcipressin; 1. DR SEQUENCE 225 AA; 25075 MW; E56B705D3CE1E3B9 CRC64;	Query Match 65.4%; Score 848; DB 1; Length 197; Best Local Similarity 88.0%; Pred. No. 3.8e-64; Matches 161; Conservative 8; Mismatches 14; Indels 0; Gaps 0; Qy 57 NSLFACNTHQSYPEEEEEEKEKEPEGLFPTYDECUTFQLFKSFRVRINSHPKSAARIE 116 Db 11 STLVACVVDVEFTENQEVKEKEPEGLFPTYDDCTVFQLFKSFRVRINSNPKSAARIE 70 Qy 117 LHETQFRGKKLPLHYAQVOTPBTGDKLHLAPPQAKQFLISPPSSPSVGKPKISDATPV 176 Db 71 LHETQFRGKKLHYAQVOTPBTGDKLHLAPPQAKQFLISPPSSPSVGKPKISDATPV 130 Qy 177 LNNDLLYAVAKLGPGEKVELHAGTESTPSVYVHCDSDMREEDPKTSPEKINKNOTRPG 236 Db 131 LNNDLLYAVAKLGPGEKVELHAGTESTPSVYVHCDSDIBBEDPKTSPEKINKNOTRPG 190 Qy 237 LPP 239 Db 191 LPP 193	RESULT 9 Q6NSN4 ID Q6NSN4 PRELIMINARY; PRT; 195 AA.

Qy	28	ICCCCDRWAVTQCFA--EFAQQLTDFPNSLFACNVHQSVFEEBESKEKFEGLFRFTY	85	CC	Name=1; IsoId=Q9UKA8-1; Sequence=Displayed;
Db	16	LQSSDQEEEENVFGENDGLDEMMDLSLPLSLFACS VHEAVFYEQEEKERFEALFTY	75	CC	Name=2;
Qy	86	DECYTFQFLFKSPRRVIRINSHPKSAARARIELHETQRGKLPYLPAQVQTPETDDKLH	145	CC	IsoId=Q9UKA8-2; Sequence=vSP_001319;
Db	76	DIQYTFQFLFKSPRRVIRINSKPEAAARARIELHESSEFHGRKLKPYAQVQSGEARDSY	135	CC	-1- TISSUE SPECIFICITY: Highest expression in heart, skeletal muscle kidney, liver and peripheral blood leukocytes. Lower expression in all other tissues.
Qy	146	LAPPQPAKQFLISPPSSPSVGKPKISATAPVINYDLYAVAKLGPKSEKYELHAGTESTPS	205	CC	-1- SIMILARITY: Belongs to the DSCR1 family.
Db	136	LPPQPQPKQFLISPPSPVGKPKQSEAMPVINYDLYCAVSKLGPKSEKYELHAGTESTPS	195	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial purposes requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Qy	206	VVVHVCDSDMREEDPKTSPKERINOTRQLPLP	238	CC	CC
Db	196	VVVHVCESETEBEDTK-NPKRITQTRPEAP	227	CC	CC
RESULT 11				CC	CC
COP3_HUMAN		STANDARD;	PRT;	241 AA.	CC
ID		Q9UKA8; Q9U7A7; Q9U7A7;			CC
AC					CC
DT	16-OCT-2001 (Rel. 40, Created)				CC
DT	16-OCT-2001 (Rel. 40, Last sequence update)				CC
DT	05-JUL-2004 (Rel. 44, Last annotation update)				CC
DB	Calciexpressin 3 (Down syndrome candidate region 1-like protein 3) (MCIP3).				CC
DE	(Myocyte-enriched calcineurin interacting protein 3) (MCIP3).				CC
GN	Name=DSCR12;				CC
OS	Homo sapiens (Human)				CC
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				CC
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				CC
OX	NCBI_TAXID=9606;				CC
RN	[1]				CC
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).				CC
RC	TISSUE=Peripheral blood, and Placenta;				CC
RX	MEDLINE=20221370; PubMed=10756093; DOI=10.1006/geno.2000.6127;				CC
RA	"A new gene family including DSCR1. Down syndrome candidate region 1 and ZAK1-like 2, a novel human member (DSCR12)." ;				CC
RT	RT				CC
RT	RT				CC
RT	RT				CC
RT	RT				CC
RN	SEQUENCE FROM N.A. (ISOFORM 1).				CC
RC	TISSUE=Brain;				CC
RX	MEDLINE=22388257; PubMed=124797932; DOI=10.1073/pnas.242603899;				CC
RA	Klauber R.D., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,				CC
RA	Altenschul S.F., Zeiberger B., Buetow K.H., Schaefer C.M., Bhat N.K.,				CC
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wong J.J., Heien P.,				CC
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				CC
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				CC
RA	Brownstein M.J., Usdin T.R., Toshimori S., Carninci P., Prange C.,				CC
RA	Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mulahay S.J.,				CC
RA	Bosak S.A., McEvans P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				CC
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				CC
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madaan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialus D.E., Schnarch A., Schein J.B., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).				CC
RN	SEQUENCE OF 66-241 FROM N.A.				CC
RA	Bagguley C.; Inhibits calcineurin-dependent transcriptional responses by binding to the catalytic domain of calcineurin A. Could play a role during central nervous system development (By similarity).				CC
CC	-1- ALTERNATIVE PRODUCTS:				CC
CC	Event=Alternative splicing; Named isoforms=2;				CC
RN	[3]				CC
RP	Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.				CC
CC	-1- FUNCTION: Inhibits calcineurin-dependent transcriptional responses by binding to the catalytic domain of calcineurin A. Could play a role during central nervous system development (By similarity).				CC
CC	-1- ALTERNATIVE PRODUCTS:				CC
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D.,				RA
RA	Klausner R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D., NCBI_TAXID=7955;				RA
RN	[1]				RA
RP	SEQUENCE FROM N.A.				RA
RC	TISSUE=Whole;				RA
DT	DOI=10.1073/pnas.242603899; PubMed=12477932; DT=25-OCT-2004 (TREMBREL: 28, Last sequence update)				RA
DT	DOI=22388257; PubMed=124797932; DT=25-OCT-2004 (TREMBREL: 28, Last annotation update)				RA
DT	DOI=10.1073/pnas.242603899; PubMed=12477932; DT=25-OCT-2004 (TREMBREL: 28, Last annotation update)				RA
OS	Brachydanio rerio (Zebrafish) (Danio rerio); Buteleostomi; Craniata; Vertebrata; Teleostei; Ostariophysi; Cypriniformes; Osteichthyes; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.				RA
OC					RA
OC					RA
OX					RA
RN	[1]				RA

		Search completed: November 16, 2005, 17:12:35
		Job time : 61.5 secs
Db	124	LHKTEFGKEMKLKYFACTLHIGSS---HLAPPNPQQLFISPPASPPVGKQVEADTPV 179
Qy	177	LNYDLILYAVAKLGPGKXYELLAGTESTPSVWVHVCSDMREEDPK---TSPKPKINQ 231
Db	180	INYDLYIAYAISKLGPGKXYEHAATDTPSVWVHVCSDQEEEEEMERMKRPKXIIQ 239
Qy	232	TRRGGLPP 239
Db	240	TRRPETP 247
RESULT 15		
	CCP1_CRICR	STANDARD;
	CCP1_ID	PRT;
	AC 03587;	197 AA.
	DT 30-MAY-2000 (Rel. 39, Created)	
	DT 30-MAY-2000 (Rel. 39, Last sequence update)	
	DT 05-JUL-2004 (Rel. 44, Last annotation update)	
	DE Calcipressin 1 (Down syndrome critical region protein 1 homolog)	
	DE (Oxidative-induced protein Adapt78).	
	GN Name=DSCR1; Synonyms=ADAPT78;	
	OS Cricetulus griseus (Chinese hamster).	
	RA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;	
	OC Cricetulus.	
	NCBI_TaxID=10029;	
	RN [1]	
	RP SEQUENCE FROM N.A.	
	MEDLINE-9732905; RX	
	Crawford D.R., Leahy K.P., Abramova N., Lan L., Wang Y., Davies K.J.;	
	RA "Hamster adapt78 mRNA is a Down syndrome critical region homologue that is inducible by oxidative stress."	
	RT Arch. Biochem. Biophys. 342:6-12 (1997).;	
	RL -i- FUNCTION: Inhibits calcineurin-dependent transcriptional responses by binding to the catalytic domain of calcineurin A. Could play a role during central nervous system development (By similarity).	
	CC -i- INDUCTION: By oxidative stress.	
	CC -i- SIMILARITY: Belongs to the DSCR1 family.	
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	CC -----	
	DR U60263; AAB68517.1; -.	
	DR InterPro; IPR06931; Calcipressin.	
	DR Pfam; PF04847; Calcipressin_1.	
	SQ SEQUENCE 197 AA; 22674 MW; OERFC68FA5826439 CRC64;	
	Query Match 47.6%; Score 617; DB 1; Length 197;	
	Best Local Similarity 62.2%; Pred. No. 1.7e-44;	
	Matches 120; Conservative 26; Mismatches 39; Indels 8; Gaps 2;	
	Qy 51 DFSDLENSFLACNVHQSVERBESKRFEGFLRTYBCVTFQLFRKFRVRINFSHIPKSA 110	
	Db 5 DFNYYNSSLIACYANGDVSESETRKEPKESFRYTDITFQYFSPKRTRINFNSPLSA 64	
Qy	111 1 ARARIELHETOFRGKCLPLYAQVQTPETDGDKLHIAHAPPAKOFLLSPPSPSYCWKPI 170	
Db	65 ADARILQHAKTEFLGKEMKLFAOTLIGGS ---HAPPNDKQFLLSPSPSPYVWQV 120	
Qy	171 SDATPUNYDLYIAYAKLGPGKXYEHAATDTPSVWVHVCSDMREEDPKTS---PK 226	
Db	121 EDATPVINYDLYIAYSKLGPGKXYEHAATDTPSVWVHVCSDQNEEEEMERMKRPK 180	
Qy	227 PKINOTRRGPLPP 239	
Db	181 PKITCOPRPEVPT 193	